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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:16:04 ; Search time 130 Seconds
(without alignments)
490.902 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 1043

Sequence: 1 LPICPGAARCVTLRDLFD.....HKIDNYLKLLKCRILHNHC 199

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1043	100.0	199	14	US-10-153-207-4
2	1043	100.0	200	10	US-09-819-094-9
3	1043	100.0	200	16	US-10-714-067-9
4	1043	100.0	227	9	US-09-815-306-1
5	1043	100.0	227	12	US-10-221-278-226
6	1043	100.0	227	14	US-10-140-293-3
7	1043	100.0	227	15	US-10-291-172-226
8	1039	99.6	228	12	US-09-065-330D-2
9	1035	99.2	200	16	US-10-449-609-1
10	1035	99.2	227	14	US-10-140-293-4
11	1035	99.2	385	16	US-10-449-609-6
12	1031	98.8	199	14	US-10-140-293-12
13	1026.5	98.4	579	16	US-10-449-609-7
14	1026.5	98.4	942	16	US-10-449-609-8
15	895	85.8	199	14	US-10-140-293-24

16	887	85.0	199	14	US-10-140-293-21	Sequence 21, Appl
17	881	84.5	199	14	US-10-140-293-22	Sequence 22, Appl
18	865	82.9	199	14	US-10-140-293-16	Sequence 16, Appl
19	863.5	82.8	198	14	US-10-140-293-30	Sequence 30, Appl
20	856	82.1	199	14	US-10-140-293-20	Sequence 20, Appl
21	792	75.9	199	14	US-10-140-293-18	Sequence 18, Appl
22	782	75.0	199	14	US-10-140-293-19	Sequence 19, Appl
23	776	74.4	199	14	US-10-140-293-28	Sequence 28, Appl
24	775	74.3	199	14	US-10-140-293-29	Sequence 29, Appl
25	772	74.0	199	14	US-10-140-293-17	Sequence 17, Appl
26	760	72.9	210	12	US-10-424-599-276669	Sequence 276669,
27	748	71.7	199	14	US-10-140-293-25	Sequence 25, Appl
28	747	71.6	199	14	US-10-140-293-26	Sequence 26, Appl
29	747	71.6	199	14	US-10-140-293-27	Sequence 27, Appl
30	737	70.7	199	14	US-10-140-293-23	Sequence 23, Appl
31	725.5	69.6	258	12	US-10-221-278-602	Sequence 602, App
32	725.5	69.6	258	15	US-10-291-172-602	Sequence 602, App
33	705	67.6	140	10	US-09-819-094-11	Sequence 11, Appl
34	705	67.6	140	16	US-10-714-067-11	Sequence 11, Appl
35	705	67.6	143	10	US-09-819-094-12	Sequence 12, Appl
36	705	67.6	143	16	US-10-714-067-12	Sequence 12, Appl
37	702	67.3	199	14	US-10-140-293-31	Sequence 31, Appl
38	690.5	66.2	198	14	US-10-140-293-32	Sequence 32, Appl
39	663	63.6	197	14	US-10-140-293-13	Sequence 13, Appl
40	657	63.0	197	14	US-10-140-293-15	Sequence 15, Appl
41	630	60.4	125	13	US-10-036-869-25	Sequence 25, Appl
42	630	60.4	253	13	US-10-036-869-27	Sequence 27, Appl
43	626	60.0	124	10	US-09-819-094-10	Sequence 10, Appl
44	626	60.0	124	16	US-10-714-067-10	Sequence 10, Appl
45	612	58.7	197	14	US-10-140-293-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

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US-10-153-207-4
; Sequence 4, Application US/10153207
; Publication No. US20030153003A1
; GENERAL INFORMATION:
; APPLICANT: James A. Wells
; TITLE OF INVENTION: GROWTH HORMONE VARIANTS
; FILE REFERENCE: 669.12-US-C7
; CURRENT APPLICATION NUMBER: US/10/153,207
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 08/479,884
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/190,723
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 07/960,227
; PRIOR FILING DATE: 1992-10-13
; PRIOR APPLICATION NUMBER: 07/875,204
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/428,066
; PRIOR FILING DATE: 1989-10-26
; PRIOR APPLICATION NUMBER: 07/264,611
; PRIOR FILING DATE: 1988-10-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-207-4
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Query Match 100.0%; Score 1043; DB 14; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.6e-101;

Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPICPGAARCVTLRDLFDRAVVLSHYIHLNLSSEMFEDKRYTHGRGFTTKAINSCHT 60

Db 1 LPICPGAARCVTLRDLFDRAVVLSHYIHLNLSSEMFEDKRYTHGRGFTTKAINSCHT 60

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; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/10/714.067
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/819.094
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076.675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046.394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-714-067-9

Query Match      100.0%; Score 1043; DB 16; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 2 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 61
Qy 61 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 120
Db 62 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 121
Qy 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 180
Db 122 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 181
Qy 181 KIDNYLKLLKCRIIHNNC 199
Db 182 KIDNYLKLLKCRIIHNNC 200

RESULT 4
US-09-815-306-1
; Sequence 1, Application US/09815306
; Patent No. US20020068043A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; TITLE OF INVENTION: BI-FUNCTIONAL CANCER TREATMENT AGENTS
; FILE REFERENCE: 035879/0120
; CURRENT APPLICATION NUMBER: US/09/815.306
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,457
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-306-1

Query Match      100.0%; Score 1043; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 29 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 88
Qy 61 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 120
Db 89 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 148
Qy 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 180
Db 149 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 208
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; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/10/714.067
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/819.094
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076.675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046.394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-714-067-9

Query Match      100.0%; Score 1043; DB 16; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
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Qy 61 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 120
Db 62 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 121
Qy 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 180
Db 122 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 181
Qy 181 KIDNYLKLLKCRIIHNNC 199
Db 182 KIDNYLKLLKCRIIHNNC 200

RESULT 2
US-09-819-094-9
; Sequence 9, Application US/09819094
; Publication No. US20030186382A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: No. US20030186382A1el Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use
; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/09/819.094
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076.675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046.394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-094-9

Query Match      100.0%; Score 1043; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.6e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 2 LPICPGGAARCVTLRDLFDRAVVLVSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 61
Qy 61 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 120
Db 62 SSLATPEDKEAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGQEAPEAILSKAVEIE 121
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Db 122 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSh 181
Qy 181 KIDNYLKLLKCRIIHNNC 199
Db 182 KIDNYLKLLKCRIIHNNC 200

RESULT 3
US-10-714-067-9
; Sequence 9, Application US/10714067
; Publication No. US20040077054A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: Novel Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use
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QY 181 KIDNYLKLLKCRIIHNNC 199
Db 209 KIDNYLKLLKCRIIHNNC 227

RESULT 5
US-10-221-278-226
; Sequence 226, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 226
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-226

Query Match 100.0%; Score 1043; DB 12; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 60
Db 29 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 88
QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 89 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148
QY 121 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 180
Db 149 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 208
QY 181 KIDNYLKLLKCRIIHNNC 199
Db 209 KIDNYLKLLKCRIIHNNC 227

RESULT 6
US-10-140-293-3
; Sequence 3, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-140-293-3

Query Match 100.0%; Score 1043; DB 14; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 60
Db 29 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 88
QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 89 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148
QY 121 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 180
Db 149 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 208
QY 181 KIDNYLKLLKCRIIHNNC 199
Db 209 KIDNYLKLLKCRIIHNNC 227

RESULT 7
US-10-291-172-226
; Sequence 226, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 226
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-226

Query Match 100.0%; Score 1043; DB 15; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 60
Db 29 LPICPGAARQCQVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 88
QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 89 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148
QY 121 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 180
Db 149 EQTKRLLEGMEIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDHS 208
QY 181 KIDNYLKLLKCRIIHNNC 199
Db 209 KIDNYLKLLKCRIIHNNC 227
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Db      209 KIDNYLKLLKCRIIHNNC 227

RESULT 8
US-09-065-330D-2
; Sequence 2, Application US/09065330D
; Publication No. US20001003662A1
; GENERAL INFORMATION:
; APPLICANT: WALKER, Ameae M.
; TITLE OF INVENTION: PROLACTIN ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 39754-0611-1CP1CP
; CURRENT APPLICATION NUMBER: US/09/065,330D
; CURRENT FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: PCT/US97/01435
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 08/594,809
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Site mutated amino acid residue where the normal
; OTHER INFORMATION: codon coding for serine is modified preferably to encode
; OTHER INFORMATION: for aspartate or glutamate, most preferably
; OTHER INFORMATION: aspartate.
US-09-065-330D-2

Query Match      99.6%; Score 1039; DB 12; Length 228;
Best Local Similarity 99.5%; Pred. No. 5.1e-101;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db      30 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 89
Qy      61 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db      90 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 149
Qy      121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDSDH 180
Db      150 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDXH 209
Qy      181 KIDNYLKLLKCRIIHNNC 199
Db      210 KIDNYLKLLKCRIIHNNC 228

RESULT 9
US-10-449-609-1
; Sequence 1, Application US/10449609
; Publication No. US20040127407A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
; FILE REFERENCE: 035879-0163
; CURRENT APPLICATION NUMBER: US/10/449,609
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/384,121
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-609-1

Db      209 KIDNYLKLLKCRIIHNNC 227

Query Match      99.2%; Score 1035; DB 16; Length 200;
Best Local Similarity 99.5%; Pred. No. 1.1e-100;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db      2 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 61
Qy      61 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db      62 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 121
Qy      121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDSDH 180
Db      122 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDSDH 181
Qy      181 KIDNYLKLLKCRIIHNNC 199
Db      182 KIDNYLKLLKCRIIHNNC 200

RESULT 10
US-10-140-293-4
; Sequence 4, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIPERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-140-293-4

Query Match      99.2%; Score 1035; DB 14; Length 227;
Best Local Similarity 99.5%; Pred. No. 1.3e-100;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db      29 LPICPGGAARCOVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 88
Qy      61 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db      89 SSLATPEDKEQAQQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148
Qy      121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDSDH 180
Db      149 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLOWADEESLSAYYNLLHCLRRDSDH 208
Qy      181 KIDNYLKLLKCRIIHNNC 199
Db      209 KIDNYLKLLKCRIIHNNC 227

RESULT 11
US-10-449-609-6
; Sequence 6, Application US/10449609
; Publication No. US20040127407A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
; TITLE OF INVENTION: FUSION PROTEINS
```

```

; FILE REFERENCE: 035879-0163
; CURRENT APPLICATION NUMBER: US/10/449,609
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/384,121
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 385
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-6

Query Match          99.2%; Score 1035; DB 16; Length 385;
Best Local Similarity 99.5%; Pred. No. 2.8e-100;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 2 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 61
Qy 61 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 120
Db 62 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 121
Qy 121 EQTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 180
Db 122 EQTKRLLEMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 181
Qy 181 KIDNYLKLKCRIIHNNNC 199
Db 182 KIDNYLKLKCRIIHNNNC 200

RESULT 12
US-10-140-293-12
; Sequence 12, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 199
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-140-293-12

Query Match          98.8%; Score 1031; DB 14; Length 199;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 196; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 1 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Qy 61 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 120
Db 61 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 120
Qy 121 EQTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 180
Db 121 EQTKRLRGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 180

; FILE REFERENCE: 035879-0163
; CURRENT APPLICATION NUMBER: US/10/449,609
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/384,121
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 942
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-8

Query Match          98.4%; Score 1026.5; DB 16; Length 579;
Best Local Similarity 99.5%; Pred. No. 4e-99;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 2 LPICPGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Qy 61 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 120
Db 61 SSLATPEDKEQAQOMQKDFLSLVLSIRSWNEPLYHLVTEVRGMQPAEALLSKAVEIE 120
Qy 121 EQTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 180
Db 121 EQTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESLSAYYNLLHCLRRDISH 180
Qy 181 KIDNYLKLKCRIIHNNNC 199
Db 181 KIDNYLKLKCRIIHNNNC 199

RESULT 14
US-10-449-609-8
; Sequence 8, Application US/10449609
; Publication No. US20040127407A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
; TITLE OF INVENTION: FUSION PROTEINS
; FILE REFERENCE: 035879-0163
; CURRENT APPLICATION NUMBER: US/10/449,609
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/384,121
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 942
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-8

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Query Match      98.4%; Score 1026.5; DB 16; Length 942;
Best Local Similarity 99.5%; Pred. No. 8e-99;
Matches 196; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 2 LPICPGGAARCOVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGR-FITKAINSCHT 60
QY 61 SSLATPEDKEAQOQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAIVEIE 120
Db 61 SSLATPEDKEAQOQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAIVEIE 120
QY 121 EOTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 121 EOTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
QY 181 KIDNYLKLLKCRITIHNNNC 199
Db 181 KIDNYLKLLKCRITIHNNNC 199

RESULT 15
US-10-140-293-24
; Sequence 24, Application US/10140293
; Publication No. US2003002283A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Unknown Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ancestral mammal
US-10-140-293-24

Query Match      85.8%; Score 895; DB 14; Length 199;
Best Local Similarity 83.4%; Pred. No. 6.5e-86;
Matches 166; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
Db 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60
QY 61 SSLATPEDKEAQOQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAIVEIE 120
Db 61 SSLATPEDKEAQOQMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQEAPEAILSKAIVEIE 120
QY 121 EOTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 121 EOTKRLLEGMEILIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
QY 181 KIDNYLKLLKCRITIHNNNC 199
Db 181 KIDNYLKLLKCRITIHNNNC 199
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 11:37:20 ; Search time 123 Seconds
(without alignments)
457.130 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPICPGARCVQLRLDFD.....HKIDNVKLLKCRLLHNNNC 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1043	100.0	199	2	AAY31764 Human pro
2	1043	100.0	199	5	ABG94847 Human pro
3	1043	100.0	200	2	AAW92258 Human ant
4	1043	100.0	227	2	AAR05231 AA sequen
5	1043	100.0	227	4	AAG78336 Human pro
6	1043	100.0	227	4	AAU78057 Novel hum
7	1043	100.0	227	7	ADD48810 Human pro
8	1043	100.0	351	2	AAR78691 Prolactin
9	1039	99.6	228	2	AAW23626 Prolactin
10	1039	99.6	228	2	AAW23620 Prolactin
11	1038	99.5	199	3	AAW78428 Human pro
12	1036	99.3	199	6	ABU09846 Human pro
13	1036	99.3	359	2	AAR05805 DHPF-prol
14	1035	99.2	227	4	AAG78337 Mutant hu
15	1034	99.1	227	1	AAW82079 Human pro
16	1028	98.6	199	6	ABU09878 Human pro
17	1022	98.0	199	2	AAW23629 Human pro
18	895	85.8	199	6	ABU09858 Ancestral
19	881	84.5	199	6	ABU09856 Horse pro
20	877	84.1	199	6	ABU09855 Camel pro
21	873	83.7	199	6	ABU09864 Ancestral
22	866	83.0	199	6	ABU09854 Pig prola
23	865	82.9	199	6	ABU09850 Finback w
24	794	76.1	240	6	ABR43658 Ovine pro
25	792	75.9	199	6	ABU09852 Cow prola

ALIGNMENTS

RESULT 1
AAY31764

ID AAY31764 standard; protein; 199 AA.

XX AC AAY31764;

DT 06-DEC-1999 (first entry)

XX DE Human prolactin.

XX KW Prolactin; human; variant; protein engineering.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT	Misc-difference	59	/note= "optionally substituted by Phe in human prolactin variant of Claim 8"
FT	Misc-difference	60	/note= "optionally substituted by Ser in human prolactin variant of Claim 8"
FT	Misc-difference	61	/note= "optionally substituted by Glu in human prolactin variant of Claim 8"
FT	Misc-difference	63	/note= "optionally substituted by Ile in human prolactin variant of Claim 8"
FT	Misc-difference	64	/note= "optionally substituted by Pro in human prolactin variant of Claim 8"
FT	Misc-difference	67	/note= "optionally substituted by Ser in human prolactin variant of Claim 8"
FT	Misc-difference	68	/note= "optionally substituted by Asn in human prolactin variant of Claim 8"
FT	Misc-difference	69	/note= "optionally substituted by Arg in human prolactin variant of Claim 8"
FT	Misc-difference	71	/note= "optionally substituted by Glu in human prolactin variant of Claim 8"
FT	Misc-difference	72	/note= "optionally substituted by Thr in human prolactin variant of Claim 8"
FT	Misc-difference	75	/note= "optionally substituted by Lys in human prolactin variant of Claim 8"

Abu09861 Sea turtle
Abu09853 Sheep pro
Abu09862 Crocodile
Abu09863 Alligator
Abu09851 Mink prol
Aar87090 Turkey pr
Aar87091 Turkey pr
Abu09859 Chicken p
Aar05699 Preprolac
Abu09860 Turkey pr
Abu09857 Asiatic e
Aau28245 Novel hum
Aaol16658 Human ext
Aaw92260 Human ant
Aaw92261 Human ant
Aaol16662 Human ext
Abu09865 Clawed fr
Abu09866 Bullfrog
Aap70504 Cattle re
Aar14599 Rat prola

FT Misc-difference 76 /note= "optionally substituted by Ser in human prolactin
FT variant of Claim 8"
FT Misc-difference 77 /note= "optionally substituted by Asn in human prolactin
FT variant of Claim 8"
FT Misc-difference 78 /note= "optionally substituted by Lys in human prolactin
FT variant of Claim 8"
FT Misc-difference 79 /note= "optionally substituted by Glu in human prolactin
FT variant of Claim 8"
FT Misc-difference 180 /note= "optionally substituted by Asp in human prolactin
FT variant of Claim 8"
FT Misc-difference 184 /note= "optionally substituted by Thr in human prolactin
FT variant of Claim 8"
FT Misc-difference 185 /note= "optionally substituted by Phe in human prolactin
FT variant of Claim 8"
FT Misc-difference 187 /note= "optionally substituted by Arg in human prolactin
FT variant of Claim 8"
XX US5955346-A.
XX
XX 21-SEP-1999.
XX
XX 07-JUN-1995; 95US-00476999.
XX
XX 28-OCT-1988; 88US-00264611.
XX 26-OCT-1989; 89US-00428066.
XX 27-APR-1992; 92US-00875204.
XX 13-OCT-1992; 92US-00960227.
XX 02-FEB-1994; 94US-00190723.
XX
XX (GETH) GENENTECH INC.
XX
XX Cunnigham BC, Wells JA;
XX
XX WPI; 1999-560495/47.
XX
XX Isolated nucleic acids encoding variants of human prolactin and placental
XX lactogen useful for identifying active domains within those proteins.
XX
XX Claim 7; Fig 2; 86pp; English.
XX
XX This is the amino acid sequence of human prolactin. The invention
XX provides a method for the systematic analysis of the structure and
XX function of polypeptides by identifying active domains which influence
XX the activity of the polypeptide with a target substance, and a method for
XX identifying the active amino acid residues within the active domain of a
XX polypeptide. It also provides polypeptide variants comprising segment-
XX substituted and residue-substituted growth hormones, prolactins and
XX placental lactogens. Claimed variants of human prolactin have 1-19 amino
XX acid substitutions when compared to the wild-type sequence, selected from
XX Q79N, T60S, S61E, L63I, A64P, E67S, D68N, K69R, Q71E, A72T, M75K, N76S,
XX Q77N, K78L, D79E, K180D, N184T, Y185F and K185R. These mutations
XX inactivate the active domains and binding sites of the protein.
XX Identifying receptor binding sites in hormones permits the rational
XX design of receptor specific variants. Nucleic acids encoding the
XX variants, expression vectors and host cells are also claimed
XX
XX Sequence 199 AA;
XX
XX Query Match 100.0%; Score 1043; DB 2; Length 199;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-93;
XX Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LPICPGAARCVTLRLDFRAVLVSHYTHNLSSEMFSEFDRKRYTHGRGFTTKAINSCHT 60
XX
XX 1 LPICPGAARCVTLRLDFRAVLVSHYTHNLSSEMFSEFDRKRYTHGRGFTTKAINSCHT 60
XX
XX Db

Qy 61 SSLATPEDKQAQMNQKDFLSLIVSLRSWNEPLVHLVTEVRGMOEAPAILSKAVEIE 120
Db 61 SSLATPEDKQAQMNQKDFLSLIVSLRSWNEPLVHLVTEVRGMOEAPAILSKAVEIE 120
Qy 121 EQTKRLLEGMLIVSOVHPETKENIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
Db 121 EQTKRLLEGMLIVSOVHPETKENIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
Qy 181 KIDNYLKLKCRTHNNNC 199
Db 181 KIDNYLKLKCRTHNNNC 199
RESULT 2
ABG94847
ID ABG94847 standard; protein; 199 AA.
XX AC ABG94847;
XX 03-DEC-2002 (first entry)
XX Human prolactin.
XX Growth hormone; placental lactogen; prolactin; active domain; hGH;
XX structure-function relationship; segment-substituted polypeptide.
XX Homo sapiens.
XX US6428954-B1.
XX 06-AUG-2002.
XX 06-JUN-1995; 95US-00483039.
XX 28-OCT-1988; 88US-00264611.
XX 26-OCT-1989; 89US-00428066.
XX 27-APR-1992; 92US-00875204.
XX 13-OCT-1992; 92US-00960227.
XX 02-FEB-1994; 94US-00190723.
XX (GETH) GENENTECH INC.
XX Wells JA, Cunnigham BC;
XX WPI; 2002-696875/75.
XX
XX Identifying active domains within cloned polypeptides of known amino acid
XX sequence by substituting analog segments into the parent polypeptide is
XX useful to determine the relationship between structure and function.
XX
XX Disclosure; Fig 2; 86pp; English.
XX
XX The invention relates to identifying an unknown active domain in a region
XX of known amino acid sequence in a parent polypeptide e.g. human growth
XX hormone (hGH) which has been cloned and has a pre-identified biological
XX activity, where the active domain interacts with a target when the parent
XX polypeptide is in its native-folded form and the interaction is
XX responsible for the biological activity comprising: (a) comparing the
XX amino acid sequence or polypeptide structure in the region of known amino
XX acid sequence of hGH with the amino acid sequence of polypeptide
XX structure in a region of known amino acid sequence of porcine growth
XX hormone (e.g. prolactin, placental lactogen or porcine growth
XX hormone) which has at least 15% homology with hGH alpha-carbon
XX coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates
XX for about 60% of the analogue sequence, where any interaction of the
XX analogue with the target is different from target interaction with hGH;
XX (b) substituting DNA encoding an analogous polypeptide segment from the
XX analogue into DNA encoding the full length hGH, and expressing a segment-
XX substituted polypeptide; (c) contacting the segment-substituted
XX polypeptide with the target to determine interaction; (d) repeating steps
XX (b) and (c) with a second analogous polypeptide segment; and (e)
XX comparing the difference between activity of the first and second segment

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:32:31 ; Search time 128 Seconds
(without alignments)
498.572 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199

Sequence: 1 LPICPGAARCVTLRDLFD.....HKIDNYLKLRHNNNC 199

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1335176 seqs, 320689617 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	100.0	199	14	US-10-153-207-4
2	199	100.0	200	16	US-09-819-094-9
3	199	100.0	200	16	US-10-714-067-9
4	199	100.0	227	9	US-09-815-306-1
5	199	100.0	227	12	US-10-221-278-226
6	199	100.0	227	14	US-10-140-293-3
7	199	100.0	227	15	US-10-291-172-226
8	178	89.4	228	15	US-09-065-330D-2
9	150	75.4	579	16	US-10-449-609-7
10	150	75.4	942	16	US-10-449-609-8
11	128	64.3	200	16	US-10-449-609-1
12	128	64.3	227	14	US-10-140-293-4
13	128	64.3	395	16	US-10-449-609-6
14	98	49.2	199	14	US-10-140-293-12
15	81	40.7	140	10	US-09-819-094-11

16	81	40.7	140	16	US-10-714-067-11	Sequence 11, Appl
17	81	40.7	143	10	US-09-819-094-12	Sequence 12, Appl
18	81	40.7	143	16	US-10-714-067-12	Sequence 12, Appl
19	68	34.2	125	13	US-10-036-869-25	Sequence 27, Appl
20	68	34.2	253	13	US-10-036-869-27	Sequence 10, Appl
21	65	32.7	124	10	US-09-819-094-10	Sequence 10, Appl
22	65	32.7	124	16	US-10-714-067-10	Sequence 10, Appl
23	36	18.1	258	12	US-10-221-278-602	Sequence 602, App
24	36	18.1	258	15	US-10-291-172-602	Sequence 602, App
25	31	15.6	198	14	US-10-140-293-30	Sequence 30, Appl
26	28	14.1	56	9	US-09-876-478-16	Sequence 16, Appl
27	26	13.1	199	14	US-10-140-293-20	Sequence 20, Appl
28	26	13.1	199	14	US-10-140-293-21	Sequence 21, Appl
29	26	13.1	199	14	US-10-140-293-24	Sequence 24, Appl
30	25	12.6	199	14	US-10-140-293-17	Sequence 17, Appl
31	25	12.6	199	14	US-10-140-293-22	Sequence 22, Appl
32	24	12.1	198	14	US-10-140-293-32	Sequence 32, Appl
33	19	9.5	199	14	US-10-140-293-26	Sequence 26, Appl
34	19	9.5	199	14	US-10-140-293-27	Sequence 27, Appl
35	17	8.5	199	14	US-10-140-293-16	Sequence 16, Appl
36	17	8.5	199	14	US-10-140-293-28	Sequence 28, Appl
37	17	8.5	199	14	US-10-140-293-29	Sequence 29, Appl
38	14	7.0	197	14	US-10-140-293-13	Sequence 13, Appl
39	13	6.5	56	9	US-09-876-478-15	Sequence 15, Appl
40	13	6.5	197	14	US-10-140-293-14	Sequence 14, Appl
41	12	6.0	21	9	US-09-815-306-22	Sequence 22, Appl
42	12	6.0	21	16	US-10-449-609-29	Sequence 29, Appl
43	12	6.0	199	14	US-10-140-293-18	Sequence 18, Appl
44	12	6.0	199	14	US-10-140-293-19	Sequence 19, Appl
45	12	6.0	199	14	US-10-140-293-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-153-207-4
; Sequence 4, Application US/10153207
; Publication NO. US20030153003A1
; GENERAL INFORMATION:
; APPLICANT: James A. Wells
; APPLICANT: Brian C. Cunningham
; TITLE OF INVENTION: GROWTH HORMONE VARIANTS
; FILE REFERENCE: 669.12-US-C7
; CURRENT APPLICATION NUMBER: US/10/153,207
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 08/479,884
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/190,723
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 07/960,227
; PRIOR FILING DATE: 1992-10-13
; PRIOR APPLICATION NUMBER: 07/875,204
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/428,066
; PRIOR FILING DATE: 1989-10-26
; PRIOR APPLICATION NUMBER: 07/264,611
; PRIOR FILING DATE: 1988-10-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-207-4

Query Match 100.0%; Score 199; DB 14; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.1e-190; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 1 LPICPGAARCVTLRDLFDRAVLISHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 60

Db 1 LPICPGAARCVTLRDLFDRAVLISHYIHNLSSEMFSEFDKRYTHGRGFIITKAINSCHT 60

QY 61 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 120
Db 61 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 120
QY 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
QY 181 KIDNYLKLKCRIIHNHNC 199
Db 181 KIDNYLKLKCRIIHNHNC 199

RESULT 2

US-09-819-094-9
; Sequence 9, Application US/09819094
; Publication No. US20030186382A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: No. US20030186382A1el Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use
; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/09/819,094
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076,675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-094-9

Query Match 100.0%; Score 199; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPICPGAARCVTLRDLFDRAVVLSHYIHNLSSEMFSEDFDKRYTHGRGFIITKAINSCHT 60
Db 2 LPICPGAARCVTLRDLFDRAVVLSHYIHNLSSEMFSEDFDKRYTHGRGFIITKAINSCHT 61
QY 61 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 120
Db 62 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 121
QY 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 122 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 181
QY 181 KIDNYLKLKCRIIHNHNC 199
Db 182 KIDNYLKLKCRIIHNHNC 200

RESULT 3

US-10-714-067-9
; Sequence 9, Application US/10714067
; Publication No. US20040077054A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: Novel Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use

; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/10/714,067
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/819,094
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076,675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-714-067-9

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Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 LPICPGAARCVTLRDLFDRAVVLSHYIHNLSSEMFSEDFDKRYTHGRGFIITKAINSCHT 61
QY 61 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 120
Db 62 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 121
QY 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 122 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 181
QY 181 KIDNYLKLKCRIIHNHNC 199
Db 182 KIDNYLKLKCRIIHNHNC 200

RESULT 4

US-09-815-306-1
; Sequence 1, Application US/09815306
; Patent No. US20020068043A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: BI-FUNCTIONAL CANCER TREATMENT AGENTS
; FILE REFERENCE: 035879/0120
; CURRENT APPLICATION NUMBER: US/09/815,306
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,457
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-306-1

Query Match 100.0%; Score 199; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.2e-190;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPICPGAARCVTLRDLFDRAVVLSHYIHNLSSEMFSEDFDKRYTHGRGFIITKAINSCHT 60
Db 29 LPICPGAARCVTLRDLFDRAVVLSHYIHNLSSEMFSEDFDKRYTHGRGFIITKAINSCHT 88
QY 61 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 120
Db 89 SSLATPEDKEAQQMKNQKDFLSIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE 148
QY 121 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 180
Db 149 EQTKRLLEGMEILVSVQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSh 208

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 13:20:38 ; Search time 424 Seconds
(without alignments)
1993.848 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPIPCGAARQCQTLDLFD.....HKIDNYLKLLKRIHNNC 199

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blos62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10735594 @CGN 1.1 885 @runat 10092004 144653 5545 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1043	100.0	603	2	AAx01694 Human ant
2	1043	100.0	833	6	ABV94102 Breast ca
3	1043	100.0	960	2	AaQ03293 Recombina
4	1043	100.0	970	7	ACA56818 Signallin
5	1043	100.0	1062	5	AAS44957 cDNA enco
6	1043	100.0	1071	2	Aaz41975 Human myo
7	1043	100.0	1100	2	AaQ96139 Prolactin
8	1036	99.3	5278	2	AAQ05168 Plasmid p

9	1034	99.1	832	1	AAx01694 Human ant
10	1033	99.0	600	2	AAx01694 Human ant
11	1031	98.8	3821	1	AAx01694 Human ant
12	1021.5	97.9	1066	7	AAx01694 Human ext
13	1006	96.5	832	2	AAx01694 Human ext
14	1002	96.1	603	2	AAx01697 Human ant
15	825	79.1	688	7	ABZ83636 Toxicolg
16	797	76.4	804	6	ABZ51716 Bovine pr
17	797	76.4	804	6	ABZ51716 Bovine pr
18	794	76.1	3828	1	AAx01694 Plasmid s
19	760.5	72.9	889	7	AAx01694 Plasmid s
20	754	72.3	600	2	AAx01694 Plasmid s
21	754	72.3	1281	2	AAx01694 Plasmid s
22	748	71.7	3926	2	AAx01694 Plasmid s
23	710	68.1	818	7	AAx01694 Plasmid s
24	705	67.6	423	2	AAx01694 Plasmid s
25	689.5	66.1	657	1	AAx01694 Plasmid s
26	667	64.0	899	2	AAx01694 Plasmid s
27	667	64.0	3735	2	AAx01694 Plasmid s
28	659	63.2	594	2	AAx01694 Plasmid s
29	656	62.9	822	1	AAx01694 Plasmid s
30	641	61.5	390	2	AAx01694 Plasmid s
31	641	61.5	771	2	AAx01694 Plasmid s
32	636	61.0	375	2	AAx01694 Plasmid s
33	636	61.0	754	2	AAx01694 Plasmid s
34	626	60.0	375	2	AAx01694 Plasmid s
35	619	59.3	681	2	AAx01694 Plasmid s
36	574	55.0	445	7	ABx39876 Bovine ES
37	568	54.1	437	2	AAx01694 Plasmid s
38	564	54.1	1290	2	AAx01694 Plasmid s
39	555	53.2	433	7	ABx46016 Bovine ES
40	548	52.5	431	7	ABx38684 Bovine ES
41	544	52.2	428	7	ABx41798 Bovine ES
42	543	52.1	435	7	ABx43432 Bovine ES
43	542	52.0	437	7	ABx42234 Bovine ES
44	535	51.3	436	7	ABx37481 Bovine ES
45	534	51.2	417	7	ABx42247 Bovine ES

ALIGNMENTS

RESULT 1

AAx01694
ID AAx01694 standard; DNA; 603 BP.

XX AAx01694;

DT 08-JUN-1999 (first entry)

XX Human anti-angiogenic hPRL Met-1Cys199 DNA.

XX Human; anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis;
XX growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
XX placental vascularisation; pregnancy; treatment; angiogenic disease;
XX tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation;
XX arthritis; atherosclerotic plaques; corneal graft neovascularisation;
XX wound healing; proliferative retinopathy; macular degeneration; trachoma;
XX granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome;
XX psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
XX ulcer; leukaemia; reproductive disorder; contraceptive agent;
XX gene therapy; pre-eclampsia; intrauterine growth retardation;
XX placental dysfunction; ss.

XX Homo sapiens.

XX X09851323-A1.

PD 19-NOV-1998.

XX 12-MAY-1998; 98WO-US009691.

PR 13-MAY-1997; 97US-0046394P.

PA (REGC) UNIV CALIFORNIA.

XX Weiner RI, Martial JA, Struman I, Taylor R;

XX WPI; 1999-045192/04.

DR P-PSDB; AAW92258.

XX New anti-angiogenic peptides - comprise N-terminal fragments of human

PT placental lactogen, human growth hormone, growth hormone variant or human

PT prolactin.

XX Example 3; Page 41; 87pp; English.

XX This invention describes novel human anti-angiogenic peptides derived

CC from 10 to 150 consecutive amino acids selected from the N-terminal end

CC of human placental lactogen (hPL), human growth hormone (hGH), growth

CC hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit

CC capillary endothelial cell proliferation and organisation (ii) inhibit

CC angiogenesis in chick chorioallantoic membrane and (iii) binds to at

CC least one specific receptor which does not bind an intact full length

CC hGH, hPL, prolactin or hGH-V. The invention also describes a method for

CC diagnosing a probable abnormality of placental vascularisation during

CC pregnancy. The peptides can be used for treating an angiogenic disease in

CC a subject, for inhibiting tumour formation or growth in a patient or for

CC modulating vascularisation of a patient's placenta. In particular, the

CC peptides can be used for preventing or treating e.g. malignant tumours,

CC angiofibroma, arteriovenous malformation, arthritic such as rheumatoid

CC arthritis, atherosclerotic plaques, corneal graft neovascularisation,

CC delayed wound healing, proliferative retinopathy such as diabetic

CC retinopathy, macular degeneration, granulomatous such as those occurring

CC in haemophilic joints, inappropriate vascularisation in wound healing

CC such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular

CC tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis,

CC pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours,

CC Kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose ulcers,

CC leukaemia, and reproductive disorders such as follicular and luteal cysts

CC and choriocarcinoma. They can also be used as contraceptive agents. DNA

CC encoding the peptides can be used in gene therapy. The measurement of

CC abnormal levels of N-terminal fragments of hGH, hGH-V, prolactin or hPL

CC can be used in assays for impairment of vascular development associated

CC with pre-eclampsia, intrauterine growth retardation, and placental

CC dysfunction

XX SQ Sequence 603 BP; 161 A; 173 C; 134 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.44e-102 Length: 603

Score: 1043.00 Matches: 199

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-735-594-1 (1-199) x AAX01694 (1-603)

Qy 1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20

Db 4 TTGCCCAFTCTCCCGCGGGCTCCCGATGCCAGGTGACCCCTCGAGACTGTGTGAC 63

Qy 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40

Db 64 CGCGCGCTGCTGCTGCCACTACATCCATACCTCTCTCAGAAATGTTCCAGGAATTC 123

Qy 41 AspIysArgTyrThrHisGlyArgGlyPheIleThrIysAlaIleAsnSerCysHisThr 60

Db 124 GATAAACGGTATACCATCGCGGGGTTCATTACCAAGGCCATCAACAGCTGCACACT 183

Qy 61 SerSerLeuAlaThrProGluAspIysGluGlnAlaGlnMetAsnGlnLysAspPhe 80

Db 184 TCTTCCCTTGACCCCGAGACAAGGAGCAAGCCCAACAGATGAATCAAAAGACTTT 243

Qy 81 LeuSerLeuIleValSerIleLeuArgSerTyrPasnGluProLeuTyrHisLeuValThr 100

Db 244 CTGAGCCTGATAGTCAGCATATTTCGGATCTCGGATGAGCCTCTGTATCATCTCGTACG 303

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120

Db 304 GAAGTAGCTGTATGCAAGAAGCCCGAGGCTATCTATCCAAAGCTGTAGAGATTGAG 363

Qy 121 GluGlnThrIysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140

Db 364 GAGCAAAACCAACGCGCTTCTAGAGGGCATGAGCTGATAGTCAGCCAGGTTCATCCGAA 423

Qy 141 ThrIysGluAsnGluIleTyrProValTyrSerGlyLeuProSerLeuGlnMetAlaAsp 160

Db 424 ACCAAAGAAATGAGATCTACCTGTCTGTCGGGACTTCCATCCCTCGAGATGGCTGAT 483

Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180

Db 484 GAAGAGTCTCGCCTTCTGCTTATTATTAACCTGTCTCCACTGCTTACGACGGGATTCAT 543

Qy 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys 199

Db 544 AAAATCGACAATTATCTCAAGCTCTCGAGTGCCGAATCATCCCAACAACTATGC 600

RESULT 2

ABV94102

ID ABV94102 standard; cDNA; 833 BP.

XX AC ABV94102;

XX 08-JAN-2003 (first entry)

XX Breast carcinoma related nucleotide sequence SEQ ID NO:93.

DE Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;

KW ss.

KW Homo sapiens.

OS WO200246467-A2.

PN 13-JUN-2002.

XX 07-DEC-2001; 2001WO-IB002811.

PR 08-DEC-2000; 2000US-0254090P.

PR 07-DEC-2001; 2001US-00007926.

XX 'IPSO-) IPSOGEN.

PA Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;

PI WPI; 2002-619023/66.

XX Novel polynucleotide library useful in molecular characterization of a

PT carcinoma, comprising a pool of polynucleotide sequences or its

PT subsequences which are either underexpressed or overexpressed in tumor

PT cells.

XX Claim 1; Page 172; 401pp; English.

XX The present invention describes a polynucleotide library (I) useful in

CC the molecular characterization of a carcinoma, comprising a pool of

CC polynucleotides or its subsequences which are either underexpressed or

CC overexpressed in tumor cells, and correspond to any of the

CC polynucleotide sequences chosen from the 468 sequences given in ABV94010

CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for

CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting

CC (MI) differentially expressed polynucleotide sequences which are

CC correlated with a cancer, involves obtaining a polynucleotide sample from

CC a patient, and reacting the polynucleotide sample obtained with a probe

CC immobilised on a solid support, where the probe comprises any combination

CC of the polynucleotide sequences of (I) or its expression products encoded

CC by polynucleotide sequences of (I), and detecting the reaction product.

CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)

GenCore version 5.1.6
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QM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 17:29:24 ; Search time 494 Seconds
(without alignments)
2026.868 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 1043

Sequence: 1 LPICGGAACQVTRDLFD.....HKIDNVYKLLKCRILHNNC 199

Scoring table:

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Xgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCI=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosun62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1043	100.0	684	15	US-10-140-293-1	Sequence 1, Appli
2	1043	100.0	833	15	US-10-007-926A-93	Sequence 93, Appl
3	1043	100.0	970	16	US-10-305-720-1416	Sequence 1416, Ap
4	1043	100.0	1062	13	US-10-221-278-38	Sequence 38, Appl
5	1043	100.0	1062	16	US-10-291-172-38	Sequence 38, Appl
6	1043	100.0	1097	15	US-10-119-428-41	Sequence 41, Appl
7	1039	99.6	832	13	US-09-065-330D-1	Sequence 1, Appli
8	1036	99.3	603	10	US-09-819-094-1	Sequence 1, Appli
9	1036	99.3	603	17	US-10-714-067-1	Sequence 1, Appli
10	1035	99.2	603	17	US-10-449-609-2	Sequence 2, Appli
11	1035	99.2	684	15	US-10-140-283-2	Sequence 2, Appli
12	1035	99.2	1158	17	US-10-449-609-5	Sequence 5, Appli
13	1002	96.1	603	10	US-09-819-094-4	Sequence 4, Appli
14	1002	96.1	603	17	US-10-714-067-4	Sequence 4, Appli
15	748	71.7	642	13	US-10-424-599-133827	Sequence 133827,
16	705	67.6	423	10	US-09-819-094-3	Sequence 3, Appli
17	705	67.6	423	17	US-10-714-067-3	Sequence 3, Appli
18	641	61.5	390	14	US-10-036-869-26	Sequence 26, Appl
19	641	61.5	771	14	US-10-036-869-28	Sequence 28, Appl
20	626	60.0	375	10	US-09-819-094-2	Sequence 2, Appli
21	626	60.0	375	17	US-10-714-067-2	Sequence 2, Appli
22	574	55.0	445	9	US-09-960-352-5041	Sequence 5041, Ap
23	568	54.5	437	9	US-09-960-352-6020	Sequence 6020, Ap
24	555	53.2	433	9	US-09-960-352-11181	Sequence 11181, A
25	548	52.5	431	9	US-09-960-352-3849	Sequence 3849, Ap
26	544	52.2	428	9	US-09-960-352-6963	Sequence 6963, Ap
27	543	52.1	435	9	US-09-960-352-8597	Sequence 8597, Ap
28	542	52.0	437	9	US-09-960-352-7399	Sequence 7399, Ap
29	535	51.3	436	9	US-09-960-352-2646	Sequence 2646, Ap
30	534	51.2	417	9	US-09-960-352-7412	Sequence 7412, Ap
31	524	50.2	438	9	US-09-960-352-4342	Sequence 4342, Ap
32	517	49.6	437	9	US-09-960-352-6489	Sequence 6489, Ap
33	515	49.4	415	9	US-09-960-352-7152	Sequence 7152, Ap
34	501	48.0	416	9	US-09-960-352-9977	Sequence 9977, Ap
35	495	47.8	406	9	US-09-960-352-14730	Sequence 14730, A
36	495	47.5	410	9	US-09-960-352-778	Sequence 778, App
37	491	47.1	433	9	US-09-960-352-5287	Sequence 5287, Ap
38	491	47.1	439	9	US-09-960-352-9982	Sequence 9982, Ap
39	491	47.1	439	9	US-09-960-352-13557	Sequence 13557, A
40	482	46.2	417	9	US-09-960-352-3145	Sequence 3145, Ap
41	479	45.9	425	9	US-09-960-352-3594	Sequence 3594, Ap
42	475	45.5	398	9	US-09-960-352-9300	Sequence 9300, Ap
43	473	45.3	424	9	US-09-960-352-9737	Sequence 9737, Ap
44	466	44.7	378	9	US-09-960-352-4347	Sequence 4347, Ap
45	463	44.4	363	9	US-09-960-352-6004	Sequence 6004, Ap

ALIGNMENTS

RESULT 1
US-10-140-293-1
; Sequence 1, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SCFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-140-293-1

Alignment Scores:

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Pred. No.: 1.59e-129 Length: 684
Score: 1043.00 Matches: 199
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-735-594-1 (1-199) x US-10-140-293-1 (1-684)
QY 1 LeuProLysCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
DB 85 TTGCCCATCTGTCCCGGGGGCTGCCGATGCCAGGTGACCTTCAGACCTGTTTGAC 144
QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
DB 145 CGCGCCGTGTCGTGTCCTACATCATCAATCAACCTCTCCTCAGAAATGTTTCAGCGAATTC 204
QY 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
DB 205 GATNAACGGTATACCCATGGCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACT 264
QY 61 SerSerLeuAlaThrProGluAspLysGluGlnGlnMetAsnGlnLysAspPhe 80
DB 265 TCTTCCCTTGCCACCCCGAAGACAGAGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 324
QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
DB 325 CTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 384
QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
DB 385 GAAGTACGTGTGTGCAAGAGAGCCCGAGGCTATCTTATCCAAAGCTGTAGAGATTGAG 444
QY 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
DB 445 GAGCAAAACCAACGGCTCTAGAGGGCATGGAGCTGATGATGATGATGATGATGATGATGAT 504
QY 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
DB 505 ACCAAAGAAATGAGATCTACCTCTGTGTCGGGACTTCCATCCCTGCAGATGGCTGAT 564
QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
DB 565 GAAGAGTCTCGCTTCTGCTTATTAACCTGCTCCACTGCTCCACTGCTCCACTGCTCCACT 624
QY 181 LysIleAspAsnTyrLeuLysLeuLysCysArgIleIleHisAsnAsnAsnCys 199
DB 625 AAAATCGACAAATTATCTCAAGCTCTGAAAGTGGCGAATCATCCACAAACAACACTGC 681

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RESULT 2

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US-10-007-926A-93
; Sequence 93, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: prolactin (PRL) gene.
US-10-007-926A-93

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Alignment Scores: 2.18e-129 Length: 833
Pred. No.: 1043.00 Matches: 199
Score: 1043.00 Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 15

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US-10-735-594-1 (1-199) x US-10-007-926A-93 (1-833)

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QY 1 LeuProLysCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
DB 89 TTGCCCATCTGTCCCGGGGGCTGCCGATGCCAGGTGACCTTCAGACCTGTTTGAC 148
QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
DB 149 CGCGCCGTGTCGTGTCCTACATCATCAATCAACCTCTCCTCAGAAATGTTTCAGCGAATTC 208
QY 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
DB 209 GATNAACGGTATACCCATGGCGGGGTTCATTACCAAGGCCATCAACAGCTGCCACT 268
QY 61 SerSerLeuAlaThrProGluAspLysGluGlnGlnMetAsnGlnLysAspPhe 80
DB 269 TCTTCCCTTGCCACCCCGAAGACAGAGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 328
QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
DB 329 CTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 388
QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
DB 389 GAAGTACGTGTGTGCAAGAGAGCCCGAGGCTATCTTATCCAAAGCTGTAGAGATTGAG 448
QY 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
DB 449 GAGCAAAACCAACGGCTCTAGAGGGCATGGAGCTGATGATGATGATGATGATGATGATGAT 508
QY 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
DB 509 ACCAAAGAAATGAGATCTACCTCTGTGTCGGGACTTCCATCCCTGCAGATGGCTGAT 568
QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
DB 569 GAAGAGTCTCGCTTCTGCTTATTAACCTGCTCCACTGCTCCACTGCTCCACTGCTCCACT 628
QY 181 LysIleAspAsnTyrLeuLysLeuLysCysArgIleIleHisAsnAsnAsnCys 199
DB 629 AAAATCGACAAATTATCTCAAGCTCTGAAAGTGGCGAATCATCCACAAACAACACTGC 685

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RESULT 3

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US-10-305-720-1416
; Sequence 1416, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1416
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 G531102
US-10-305-720-1416

Alignment Scores:

Pred. No.: 2,78e-129 Length: 970
Score: 1043.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-735-594-1 (1-199) x US-10-305-720-1416 (1-970)

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QY 1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrIleuArgAspLeuPheAsp 20
Db 226 TTGCCCATCTGTCCCGGGGGGTGCCGATGCCAGTGCAGCTTCCGACCTGTTTGAC 285
QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db 286 CGCGCGTGTCTGTCCCACTACATCCATAACCTCTCTCAGAAATGTTACGCGAATTC 345
QY 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 346 GATAAACGGTATACCCATGCCGGGGTTCATTTACCAAGCCCAACAGCTGCCACACT 405
QY 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
Db 406 TCTTCCCTTGGCCACCCCGAAGCAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 465
QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisIleuValThr 100
Db 466 CTGAGCCTGATAGTCAGCATATTGCCATCCTGGAATGAGCCTCTGATCATCTGGTCAG 525
QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db 526 GAAGTACGTGGTATGCAAGAGCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG 585
QY 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db 586 GAGCAAAACAAACGGCTTCTAGAGGCGATGGAGCTGATAGTCAGCAGGTTTCATCTGAA 645
QY 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db 646 ACCAAAGAAAATGAGATCTACCTGTCTGTGCGGACTTCCATCCCTGCAGATGGCTGAT 705
QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
Db 706 GAAGAGTCTCGCCTTTCTGCTTTATTATTAACCTGCTCCACTGCCCTACGAGGGATTACAT 765
QY 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
Db 766 AAAATCGACAATTATCTCAAGCTCTTGAAGTGGCGGAATCATCCACAACAACACTGC 822
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RESULT 4

US-10-221-278-38

; Sequence 38, Application US/10221278

; Publication No. US20040034208A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 21272-045

; CURRENT APPLICATION NUMBER: US/10/221,278

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 09/693,267

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 09/665,363

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: 09/616,847

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 09/596,193

; PRIOR FILING DATE: 2000-06-17

; PRIOR APPLICATION NUMBER: 09/574,454

; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 38
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)..(820)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1062)
; OTHER INFORMATION: n = a,t,c or g
US-10-221-278-38

Alignment Scores:

Pred. No.: 3,22e-129 Length: 1062
Score: 1043.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-735-594-1 (1-199) x US-10-221-278-38 (1-1062)

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QY 1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrIleuArgAspLeuPheAsp 20
Db 224 TTGCCCATCTGTCCCGGGGGGTGCCGATGCCAGTGCAGCTTCCGACCTGTTTGAC 283
QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db 284 CGCGCGTGTCTGTCCCACTACATCCATAACCTCTCTCAGAAATGTTACGCGAATTC 343
QY 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 344 GATAAACGGTATACCCATGCCGGGGTTCATTTACCAAGCCCAACAGCTGCCACACT 403
QY 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
Db 404 TCTTCCCTTGGCCACCCCGAAGCAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 463
QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisIleuValThr 100
Db 464 CTGAGCCTGATAGTCAGCATATTGCCATCCTGGAATGAGCCTCTGATCATCTGGTCAG 523
QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db 524 GAAGTACGTGGTATGCAAGAGCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG 583
QY 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db 584 GAGCAAAACAAACGGCTTCTAGAGGCGATGGAGCTGATAGTCAGCAGGTTTCATCTGAA 643
QY 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db 644 ACCAAAGAAAATGAGATCTACCTGTCTGTGCGGACTTCCATCCCTGCAGATGGCTGAT 703
QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
Db 704 GAAGAGTCTCGCCTTTCTGCTTTATTATTAACCTGCTCCACTGCCCTACGAGGGATTACAT 763
QY 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
Db 764 AAAATCGACAATTATCTCAAGCTCTTGAAGTGGCGGAATCATCCACAACAACACTGC 820
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RESULT 5

US-10-291-172-38

; Sequence 38, Application US/10291172

; Publication No. US20030228584A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

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; TITLE OF INVENTION: No. US20030228584A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 38
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)..(820)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1062)
; OTHER INFORMATION: n = a,t,c or g
US-10-291-172-38

Alignment Scores:
Pred. No.: 3.22e-129 Length: 1062
Score: 1043.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-735-594-1 (1-199) x US-10-291-172-38 (1-1062)

Qy 1 LeuProtleCysProGlyGlyAlaAlaAArgCysGlnValThrLeuArgAspLeuPheAsp 20
Db 224 TTGCCCATCTGTCCCGGGGGTCCCGATGCCAGTGACCTTCGAGACCTGTTGAC 283
Qy 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db 284 CGCGCCGCTGCTCTCCACTACATCCATAACCTCTCTCCTCAGAAATGTTTCAGCGAATTC 343
Qy 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 344 GATAAACGGTATACCATGGCGGGGGTTCTATTACCAAGGCCATCAACAGCTGCCACT 403
Qy 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
Db 404 TCTTCCCTTGCCACCCCGAAGCAAGGAGCAAGCCCAACAGATGAATCAAAAGACTTT 463
Qy 81 LeuSerLeuIleValSerIleuArgSerThrPasnGluProLeuTyrHisLeuValThr 100
Db 464 CTGAGCCTGATAGTCAGCATATTGCGATTCCTGGAATGAGCCTCTGTATCATCTGTCACG 523
Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db 524 GAAGTAGTGTATGCAAGAAGCCCCCGAGGCTATCTTATCAAGCTGTAGAGATTGAG 583
Qy 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db 584 GAGCAAAACCAACGGCTTCTAGAGGGCATGCGATGATGATGATGATGATGATGATGATGAT 643
Qy 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db 644 ACCAAAGAAATAGATCTACCTGTCTGGTGGGACTTCCATCCCTGCAGATGGCTGAT 703
Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
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Db 704 GAAGAGTCTCGCTTCTGCTTATATATACTGCTCCACTGCTACGAGGGATTACAT 763
Qy 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
Db 764 AAAATCGACAATTATCTCAAGCTCCTGAAGTCCGAATCATCCACAACAACAACTGC 820

RESULT 6
US-10-119-428-41
; Sequence 41, Application US/10119428
; Publication No. US20030165881A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehrman, Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Ma, Yunding
; APPLICANT: Zhou, Ping
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030165881A1e1 Nucleic Acids and
; FILE REFERENCE: 789CIP2
; CURRENT APPLICATION NUMBER: US/10/119,428
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 41
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)..(858)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1097)
; OTHER INFORMATION: n = a,t,c or g
US-10-119-428-41

Alignment Scores:
Pred. No.: 3.39e-129 Length: 1097
Score: 1043.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-735-594-1 (1-199) x US-10-119-428-41 (1-1097)

Qy 1 LeuProtleCysProGlyGlyAlaAlaAArgCysGlnValThrLeuArgAspLeuPheAsp 20
Db 259 TTGCCCATCTGTCCCGGGGGTCCCGATGCCAGTGACCTTCGAGACCTGTTGAC 318
Qy 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db 319 CGCGCCGCTGCTCTCCACTACATCCATAACCTCTCTCCTCAGAAATGTTTCAGCGAATTC 378
Qy 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 379 GATAAACGGTATACCATGGCGGGGGTTCTATTACCAAGGCCATCAACAGCTGCCACT 438
Qy 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
```


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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 18:15:09 ; Search time 422 Seconds
(without alignments)
2003.297 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199
Sequence: 1 LPICPGGAARQCQTLRLDLD.....HKIDNYLKLLKCRIIHNNC 199

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6745146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-O=/cpn2.1/USPTO.spool_p/DEV=xlpl
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10735594 @CGN 1 1 885 @runat 10092004 144725 5879 -NCPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	100.0	603	2 AAX01694	Aax01694 Human ant
2	199	100.0	833	6 ABV94102	Abv94102 Breast ca
3	199	100.0	960	2 AAQ03293	Aaq03293 Recombina
4	199	100.0	970	7 ACA56818	Aca56818 Signallin
5	199	100.0	1062	5 AAS44957	Aas44957 cDNA enco
6	199	100.0	1071	2 AAZ41975	Aaz41975 Human myo
7	199	100.0	1100	2 AAQ96139	Aaq96139 Prolactin
8	185	93.0	5278	2 AAQ05168	Aaq05168 Plasmid p

9	181	91.0	3621	1 AAN60847	Aan60847 Human pre
10	143	71.9	889	7 AAL51963	Aal51963 Human ext
c 11	136	68.3	688	7 ABZ83636	Abz83636 Toxicolog
12	136	68.3	1066	7 AAL51964	Aal51964 Human ext
13	124	62.3	390	2 AAX58737	Aax58737 DNA enco
14	124	62.3	771	2 AAX58738	Aax58738 DNA enco
15	124	62.3	832	1 AAN80115	Aan80115 Human pre
16	123	61.8	375	2 AAX01695	Aax01695 Human pro
17	123	61.8	754	2 AAV10506	Aav10506 Human con
18	122	61.3	600	2 AAT74325	Aat74325 cDNA enco
19	81	40.7	423	2 AAX01696	Aax01696 Human ant
20	81	40.7	603	2 AAX01697	Aax01697 Human ext
21	76	38.2	818	7 AAL51960	Aal51960 Human ext
22	65	32.7	375	2 AAX01695	Aax01695 Human ant
23	63	31.7	309	3 AAC72604	Aac72604 Single nu
24	60	30.2	309	3 AAC72598	Aac72598 Single nu
25	59	29.6	282	3 AAT72601	Aat72601 Single nu
26	57	28.6	832	2 AAT74333	Aat74333 cDNA enco
27	48	24.1	282	3 AAC72595	Aac72595 Single nu
28	40	20.1	278	3 AAC72607	Aac72607 Single nu
29	20	10.1	60	6 AEN43525	Abn43525 Human spl
30	19	9.5	445	7 ABX39876	Abx39876 Bovine ES
31	19	9.5	600	2 AAT03456	Aat03456 Turkey pr
32	19	9.5	1281	2 AAT03457	Aat03457 Turkey pr
33	14	7.0	594	2 AAT74324	Aat74324 cDNA enco
34	14	7.0	822	1 AAN80114	Aan80114 Rat prepr
35	14	7.0	899	2 AAQ14451	Aaq14451 Rat prola
c 36	14	7.0	3735	2 AAQ14452	Aaq14452 Rat prola
c 37	13	6.5	48	6 ABS73117	Abv73117 Human gro
38	13	6.5	443	6 ABV94100	Abv94100 Breast ca
39	13	6.5	681	2 AAQ13553	Aaq13553 Prolactin
40	12	6.0	47	6 ABS73116	Abv73116 Human gro
41	12	6.0	47	9 ADE82299	Ade82299 XbaI-BstE
42	12	6.0	234	7 ABX41778	Abx41778 Bovine ES
43	12	6.0	292	7 ABX48868	Abx48868 Bovine ES
44	12	6.0	299	7 ABX44819	Abx44819 Bovine ES
45	12	6.0	312	7 ABX49800	Abx49800 Bovine ES

ALIGNMENTS

RESULT 1
AAX01694
ID AAX01694 standard; DNA; 603 BP.
XX
AC AAX01694;
XX
XX
DT 08-JUN-1999 (first entry)
XX
DE Human anti-angiogenic hPRL Met-1Cys199 DNA.
XX

Human; anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis;
growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
placental vascularisation; pregnancy; treatment; angiogenic disease;
tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation;
arthritis; atherosclerotic plaques; corneal graft neovascularisation;
wound healing; proliferative retinopathy; macular degeneration; trachoma;
granulation; glaucoma; ocular; uveitis; fracture; Osher-Weber syndrome;
psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
ulcer; leukaemia; reproductive disorder; contraceptive agent;
gene therapy; pre-eclampsia; intrauterine growth retardation;
placental dysfunction; ss.

XX Homo sapiens.
XX
XX WO9851323-A1.
XX
XX 19-NOV-1998.
XX
XX 12-MAY-1998; 98WO-US009691.
XX
XX 13-MAY-1997; 97US-0046394P.
XX

PA (REGC) UNIV CALIFORNIA.
 XX Weiner RI, Martial JA, Struman I, Taylor R;
 PI WPI; 1999-045192/04.
 XX P-PSDB; AAW92258.
 DR
 XX New anti-angiogenic peptides - comprise N-terminal fragments of human
 PT placental lactogen, human growth hormone, growth hormone variant or human
 FT prolactin.
 XX
 XX Example 3; Page 41; 87pp; English.
 PS
 XX This invention describes novel human anti-angiogenic peptides derived
 CC from 10 to 150 consecutive amino acids selected from the N-terminal end
 CC of human placental lactogen (hPL), human growth hormone (hGH), growth
 CC hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit
 CC capillary endothelial cell proliferation and organisation (ii) inhibit
 CC angiogenesis in chick chorioallantoic membrane and (iii) binds to at
 CC least one specific receptor which does not bind an intact full length
 CC hGH, hPL, prolactin or hGH-V. The invention also describes a method for
 CC diagnosing a probable abnormality of placental vascularisation during
 CC pregnancy. The peptides can be used for treating an angiogenic disease in
 CC a subject, for inhibiting tumour formation or growth in a patient or for
 CC modulating vascularisation of a patient's placenta. In particular, the
 CC peptides can be used for preventing or treating e.g. malignant tumours,
 CC angiofibroma, arteriovenous malformation, arthritic such as rheumatoid
 CC arthritis, atherosclerotic plaques, corneal graft neovascularisation,
 CC delayed wound healing, proliferative retinopathy such as diabetic
 CC retinopathy, macular degeneration, granulations such as those occurring
 CC in haemophilic joints, inappropriate vascularisation in wound healing
 CC such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular
 CC tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis,
 CC pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours,
 CC Kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose ulcers,
 CC leukaemia, and reproductive disorders such as follicular and luteal cysts
 CC and choriocarcinoma. They can also be used as contraceptive agents. DNA
 CC encoding the peptides can be used in gene therapy. The measurement of
 CC abnormal levels of N-terminal fragments of hGH, hGH-V, prolactin or hPL
 CC can be used in assays for impairment of vascular development associated
 CC with pre-eclampsia, intrauterine growth retardation, and placental
 CC dysfunction
 XX
 SQ Sequence 603 BP; 161 A; 173 C; 134 G; 135 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.38e-192 Length: 603
 Score: 199.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-735-594-1 (1-199) x AAX01694 (1-603)
 QY 1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
 DB 4 TTGCCCCATGTCCCGCGGGGCTGCCCGGATGCCAGGTGACCTTCGAGACCTGTGTGAC 63
 QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
 DB 64 CGCGCGCTGCTGCTGCCACTACATCATCACTCTCTCCAGAAATGTTTCAGGAATTC 123
 QY 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
 DB 124 GATAAAGCGTATACCATGCGCGGGGTTTCATTACCAAGGCCATCAACAGCTGCCCACT 183
 QY 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnGlnMetAsnGlnLysAspPhe 80
 DB 184 TCTTCCCTTGCCACCCCGAGACACAGGACAGCCCAACAGATGAATCAAAAGACTTT 243
 QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100

Db 244 CTGAGCCTGATAGTCAGCATATTGCGATCTCGAATGAGCCTCTGTATCATCTGTGTCACG 303
 QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
 Db 304 GAAGTACGTGGTATGCAAGAAGCCCGAGGCTATCTCTATCCAAAGCTGTAGAGATTGAG 363
 QY 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
 Db 364 GAGCAAAACCAACCGGCTTCTAGAGGGCATGGAGCTGATAGTCAGCCAGGTTCACTCTGAA 423
 QY 141 ThrLysGluAsnGluIleTyrProValTyrSerGlyLeuProSerLeuGlnMetAlaAsp 160
 Db 424 ACCAAGAAATGAGATCTACCTGTCTGTCGGACTTCCATCCCTCGAGATGGCTGAT 483
 QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
 Db 484 GAAGAGTCTCGCTTCTGCTTATTATTAACCTCTCCACTGCTAGCCAGGGATTACAT 543
 QY 181 LysIleAspAsnTyrLeuLysLeuLysCysArgIleIleHisAsnAsnAsnCys 199
 Db 544 AAATCGCAATATCTCAGCTCTCGAAGTCCGGAATCATCCACAAACAACACTGC 600

RESULT 2
 ABV94102
 ID ABV94102 standard; cDNA; 833 BP.
 XX ABV94102;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Breast carcinoma related nucleotide sequence SEQ ID NO:93.
 XX
 KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
 XX ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200246467-A2.
 XX
 XX 13-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-1B002811.
 XX
 PR 08-DEC-2000; 2000US-0254090P.
 PR 07-DEC-2001; 2001US-00007926.
 XX
 XX (IPSO-) IPSOGEN.
 PA Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
 PI
 XX WPI; 2002-619023/66.
 DR
 XX Novel polynucleotide library useful in molecular characterization of a
 PT carcinoma, comprising a pool of polynucleotide sequences or its
 PT subsequences which are either underexpressed or overexpressed in tumor
 PT cells.
 XX
 PS Claim 1; Page 172; 401pp; English.
 XX
 CC The present invention describes a polynucleotide library (I) useful in
 CC the molecular characterization of a carcinoma, comprising a pool of
 CC polynucleotides or its subsequences which are either underexpressed or
 CC overexpressed in tumour cells, and correspond to any of the
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
 CC to ABV94477. Also described: (i) a polynucleotide array (ii) useful for
 CC the prognosis or diagnostic of tumour, comprising (i); and (2) detecting
 CC (M1) differentially expressed polynucleotide sequences which are
 CC correlated with a cancer, involves obtaining a polynucleotide sample from
 CC a patient, and reacting the polynucleotide sample obtained with a probe
 CC immobilised on a solid support, where the probe comprises any combination
 CC of the polynucleotide sequences of (i) or its expression products encoded
 CC by polynucleotide sequences of (i), and detecting the reaction product.
 CC (i) have cytostatic activities and can be used as anti-tumour agents. (i)

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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:06:10 ; Search time 40 Seconds
(without alignments)

478.553 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 1043

Sequence: 1 LPICPGAAACQVTLRDLPD.....HKIDNVKLLKCRITNNNC 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043	100.0	227	1 LCHU	prolactin precursor
2	1031	98.8	228	2 A61402	prolactin precursor
3	887	85.0	199	2 S15131	prolactin - Arabia
4	877	84.1	229	1 LCPG	prolactin precursor
5	876	84.0	199	1 LCHO	prolactin - horse
6	867	83.1	229	2 JC4631	prolactin precursor
7	861	82.6	199	2 PN0128	prolactin - sei wh
8	797	76.4	229	1 LCBO	prolactin precursor
9	796	76.3	229	1 LC5H	prolactin precursor
10	796	76.3	229	2 I83982	prolactin - goat
11	790.5	75.8	198	1 A60620	prolactin - green
12	772	74.0	175	2 S18882	prolactin - Americ
13	770	73.8	229	2 A60972	prolactin precursor
14	754	72.3	229	2 A61133	prolactin precursor
15	737	70.7	199	2 JS0430	prolactin - elepha
16	690.5	66.2	207	2 A60969	prolactin precursor
17	667	64.0	226	1 LCRT	prolactin precursor
18	657	63.0	226	2 A49159	prolactin - golden
19	621	59.5	228	1 LCMS	prolactin precursor
20	601.5	57.7	200	2 S34604	prolactin - marble
21	494	47.4	134	2 I51233	prolactin - Japane
22	468	44.9	236	2 A37930	prolactin - lactogen
23	464.5	44.5	221	2 A41407	prolactin - lactogen
24	443	42.5	236	2 A40143	prolactin - lactogen
25	417.5	40.0	222	2 A26489	prolactin-like pro
26	416.5	39.9	238	2 B36284	prolactin-related
27	415.5	39.8	267	2 A34078	prolactin - lactogen
28	402.5	38.6	221	2 A25951	prolactin-related
29	387	37.1	238	2 A31417	prolactin-related

RESULT 1

LCHU

prolactin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1979 #sequence revision 23-Oct-1981 #text change 08-Dec-2000

C:Accession: A90998; A53318; A28867; PN0089; A92762; A92177; A01505

R:Truong, A.T.; Duez, C.; Belayew, A.; Renard, A.; Pictet, R.; Bell, G.I.; Martial, J.A.

EMBO J. 3, 429-437, 1984

A:Title: Isolation and characterization of the human prolactin gene.

A:Reference number: A90998; MUID:84182507; PMID:6325171

A:Accession: A90998

A:Molecule type: DNA

A:Residues: 1-227 <TRU>

R:Cooke, N.E.; Coit, D.; Shine, J.; Baxter, J.D.; Martial, J.A.

J. Biol. Chem. 256, 4007-4016, 1981

A:Title: Human prolactin: cDNA structural analysis and evolutionary comparisons.

A:Reference number: A92318; MUID:8168179; PMID:6260780

A:Accession: A92318

A:Molecule type: mRNA

A:Residues: 1-227 <COO>

A:Cross-references: GB:V00566; GB:J00299; NID:g34210; PIDN:CAA23829.1; PID:g34211

R:Takahashi, H.; Nabeshima, Y.; Nabeshima, Y.; Ogata, K.; Takeuchi, S.

J. Biochem. 95, 1491-1499, 1984

A:Title: Molecular cloning and nucleotide sequence of DNA complementary to human decidua

A:Reference number: A28867; MUID:84264464; PMID:6146607

A:Accession: A28867

A:Molecule type: mRNA

A:Residues: 1-205, 'H', 207-227 <TAK>

A:Cross-references: EMBL:M29386

A:Note: the authors translated the codon CAT for residue 206 as Asp

R:Mertvetsov, N.P.; Golovin, S.Y.; Zelenin, S.M.; Morozova, T.V.; Karginov, V.A.; Chekhr

Bioorg. Khim. 13, 1687-1690, 1987

A:Title: Synthesis, cloning and sequencing of cDNA complementary to mRNA of prolactin fi

A:Reference number: PN0089; MUID:88221681; PMID:3450284

A:Accession: PN0089

A:Molecule type: mRNA

A:Residues: 45-227 <MER>

A:Experimental source: pituitary gland

A:Note: the authors translated the codon AAC for residue 15 as Asp

R:Shome, B.; Parlow, A.F.

J. Clin. Endocrinol. Metab. 45, 1112-1115, 1977

A:Title: Human pituitary prolactin (hPRL): the entire linear amino acid sequence.

A:Reference number: A92762; MUID:78046207; PMID:925136

A:Accession: A92762

A:Molecule type: protein

A:Residues: 29-109, 'VS', 112, 'L', 115-132, 'X', 134-171, 'D', 173-189, 'SE', 192-227 <SHO>

R:Jacobs, J.M.; Niall, H.D.

J. Biol. Chem. 250, 3629-3636, 1975

A:Title: High sensitivity automated sequence determination of polypeptides.

A:Reference number: A92177; MUID:75151509; PMID:1126929

A:Accession: A92177

A:Molecule type: protein

A;Residues: 29-52, 'L' <JAC>

C;Genetics:

A;Gene: GDB:PRL

A;Cross-references: GDB:119517; OMIM:176760

A;Map position: 6p22.2-6p22.1

A;Insertions: 9/3; 68/3; 104/3; 164/3

C;Superfamily: prolactin

C;Keywords: anterior pituitary; hormone; lactation; placenta

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-227/Product: prolactin #status experimental <MAT>

F;32-39,86-202,219-227/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1043; DB 1; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.8e-78;

Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60

Db 29 LPICPGGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 88

QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLHYLHVTVEVGMQAPPAILSKAVEIE 120

Db 89 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLHYLHVTVEVGMQAPPAILSKAVEIE 148

QY 121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 180

Db 149 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 208

QY 181 KIDNYLKLLKCRITIHNNNC 199

Db 209 KIDNYLKLLKCRITIHNNNC 227

RESULT 2

A61402

C;Species: prolactin precursor, placental (clone 204) - human

C;Species: Homo sapiens (man)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Feb-1997

C;Accession: A61402

F;Hiraoka, Y.; Tatsumi, K.; Shiozawa, M.; Aiso, S.; Fukasawa, T.; Yasuda, K.; Miyai, K.

Mol. Cell. Endocrinol. 75, 71-80, 1991

A;Title: A placenta-specific 5' non-coding exon of human prolactin.

A;Reference number: A61402; MUID:91267286; PMID:2050267

A;Accession: A61402

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-228 <HIR>

C;Superfamily: prolactin

C;Keywords: alternative splicing

F;87-203,220-228/Disulfide bonds: #status predicted

Query Match 98.8%; Score 1031; DB 2; Length 228;

Best Local Similarity 99.5%; Pred. No. 3.7e-77;

Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60

Db 30 LPICPGGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 89

QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLHYLHVTVEVGMQAPPAILSKAVEIE 120

Db 90 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLHYLHVTVEVGMQAPPAILSKAVEIE 149

QY 121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 180

Db 150 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 209

QY 181 KIDNYLKLLKCRITIHNNNC 199

Db 210 KIDNYLKLLKCRITIHNNNC 228

RESULT 3

S15131

prolactin - Arabian camel

C;Species: Camelus dromedarius (Arabian camel)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-May-2000

C;Accession: S15131; A60513

R;Martinat, N.; Huet, J.C.; Nespoulous, C.; Combarnous, Y.; Pernollet, J.C.

Biochim. Biophys. Acta 1077, 339-345, 1991

A;Title: Determination of the primary and secondary structures of the dromedary (Camelus dromedarius) prolactin

A;Reference number: S15131; MUID:91230144; PMID:2029533

A;Accession: S15131

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-199 <MAR>

R;Martinat, N.; Anouassi, A.; Huet, J.C.; Pernollet, J.C.; Combarnous, Y.

Comp. Biochem. Physiol. B 97, 667-674, 1990

A;Title: Purification and characterization of glycosylated and non-glycosylated forms of dromedary prolactin

A;Reference number: A60513; MUID:91199560; PMID:2085952

A;Accession: A60513

A;Molecule type: protein

A;Residues: 1-40 <MA2>

C;Superfamily: prolactin

C;Keywords: anterior pituitary; hormone; lactation; placenta

Query Match 85.0%; Score 887; DB 2; Length 199;

Best Local Similarity 81.4%; Pred. No. 1.9e-65;

Matches 162; Conservative 22; Mismatches 15; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60

Db 1 LPICPGAVNCQVSLRDLFRAVVLSHYIHLNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60

QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLHYLHVTVEVGMQAPPAILSKAVEIE 120

Db 61 SSLSTPEDKEQAQOIHEDLNLVLRVSWNDPLHYLHVTVEVGMQAPPAILSKAVEIE 120

QY 121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 180

Db 121 EQTKRLLEGMLIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSD 180

QY 181 KIDNYLKLLKCRITIHNNNC 199

Db 181 KIDNYLKLLKCRITIHNNNC 199

RESULT 4

LCPG

prolactin precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 24-Apr-1984 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999

C;Accession: S04077; A60971; A01507

R;Schulz-Aellen, M.F.; Schmid, E.; Movva, R.N.

Nucleic Acids Res. 17, 3295, 1989

A;Title: Nucleotide sequence of porcine prolactin cDNA.

A;Reference number: S04077; MUID:89263739; PMID:2726463

A;Accession: S04077

A;Molecule type: mRNA

A;Residues: 1-229 <SCH>

A;Cross-references: EMBL:X14068; NID:g2082; PIDN:CAA32231.1; PID:g2083

R;Kato, Y.; Hirai, T.; Kato, T.

J. Mol. Endocrinol. 4, 135-142, 1990

A;Title: Molecular cloning of cDNA for porcine prolactin precursor.

A;Reference number: A60971; MUID:90262633; PMID:2344390

A;Accession: A60971

A;Molecule type: mRNA

A;Residues: 1-3,'R',5,'X',7-42,'V',44-229 <KAT>

R;Li, C.H.

Int. J. Pept. Protein Res. 8, 205-224, 1976

A;Title: Studies on pituitary lactogenic hormone. The primary structure of the porcine prolactin

A;Reference number: A91770; MUID:76189476; PMID:1270193

A;Accession: A01507

A;Molecule type: protein

A;Residues: 31-42,'V',44-151,'B',153-225,'N',227-229 <LIC>

C;Superfamily: prolactin

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 11:39:59 ; Search time 24 Seconds
(without alignments)
431.748 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 1043

Sequence: 1 LPICPGAAQCQVTLRDLPD.....HKIDNYLKLLKCRHNNNC 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1043	100.0	227	1 PRL_HUMAN	P01236 homo sapien
2	1029	98.7	227	1 PRL_MACMU	P55151 macaca mula
3	887	85.0	199	1 PRL_CAMDR	P22393 camelus dro
4	880	84.4	229	1 PRL_PIG	P01238 sus scrofa
5	876	84.0	199	1 PRL_HORSE	P12420 equus caball
6	874	83.8	227	1 PRL_RABIT	Q28632 oryctolagus
7	867	83.1	229	1 PRL_FELCA	P46403 felis silve
8	861	82.6	199	1 PRL_BALBO	P33089 balaeonopter
9	857	82.2	228	1 PRL_TRIVU	O62781 trichosurus
10	852	81.7	193	1 PRL_MUSVI	P29234 mustela vis
11	847	81.2	228	1 PRL_MONDO	O62819 monodelphis
12	798	76.5	229	1 PRL_CAPHI	Q28318 capra hircu
13	797	76.4	229	1 PRL_BOVIN	P01239 bos taurus
14	796	76.3	229	1 PRL_SHEEP	P01240 ovis aries
15	790.5	75.8	198	1 PRL_CHEMY	P33090 chelonina my
16	777	74.5	199	1 PRL2_ALIMI	P35752 alligator m
17	776	74.4	199	1 PRL2_CRONO	P35754 crocodylus
18	772	74.0	199	1 PRL1_ALLMI	P35751 alligator m
19	771	73.9	199	1 PRL1_CRONO	P35753 crocodylus
20	770	73.8	229	1 PRL_CHICK	P14676 gallus gall
21	754	72.3	229	1 PRL_MELGA	P17572 meleagris g
22	737	70.7	199	1 PRL_LOXAF	P10765 loxodonta a
23	667	64.0	226	1 PRL_RAT	P01237 rattus norv
24	657	63.0	226	1 PRL_MESAU	P37884 mesocricetu
25	621	59.5	226	1 PRL_MOUSE	P06879 mus musculu
26	609.5	58.4	200	1 PRL_PROAT	P33091 protopterus
27	494	47.4	134	1 PRL_BURJA	P43001 bufo japoni
28	470	45.1	236	1 PRL1_BOVIN	P09611 bos taurus
29	464.5	44.5	221	1 PRL2_MESAU	P14059 mesocricetu
30	443	42.5	236	1 PRL_SHEEP	P16038 ovis aries
31	417.5	40.0	222	1 PRL2_MOUSE	P09586 mus musculu
32	416.5	39.9	238	1 PRL2_BOVIN	P19159 bos taurus
33	415.5	39.8	267	1 PRL2_BOVIN	P12401 bos taurus

RESULT 1

PRL_HUMAN

ID	PRL_HUMAN	STANDARD;	PRT;	227 AA.
AC	P01236; Q15199; Q92996;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Prolactin precursor (PRL).			
GN	PRL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84182507; PubMed=6325171;			
RA	Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,			
RA	Martial J.A.;			
RT	"Isolation and characterization of the human prolactin gene.";			
RL	EMBO J. 3:429-437(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81168179; PubMed=6260780;			
RA	Cooke N.B., Coit D., Shine J., Baxter J.D., Martial J.A.;			
RT	"Human prolactin. cDNA structural analysis and evolutionary			
RT	comparisons";			
RL	J. Biol. Chem. 256:4007-4016(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91267286; PubMed=2050267;			
RA	Hiraoka Y., Tatsumi K., Shiozawa M., Aiso S., Fukasawa T., Yasuda K.,			
RA	Miyai K.;			
RT	"A placenta-specific 5' non-coding exon of human prolactin.";			
RL	Mol. Cell. Endocrinol. 75:71-80(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Aitschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			

P09321 rattus norv
P05402 bos taurus
P04789 mus musculu
P18121 mus musculu
P34207 rattus norv
P24800 rattus norv
P18917 bos taurus
P12402 bos taurus
P21702 rattus norv
P09320 rattus norv
P04095 mus musculu
P18918 mus musculu

ALIGNMENTS

```
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP SEQUENCE OF 11-227 FROM N.A.
RX MEDLINE=84264464; PubMed=6146607;
RA Takahashi H., Nabeshima Y., Nabeshima Y., Ogata K., Takeuchi S.;
RT "Molecular cloning and nucleotide sequence of DNA complementary to
RL human decidal prolactin mRNA." ;
RN J. Biochem. 95:1491-1499(1984).
[6]
RP SEQUENCE OF 11-201 FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=97411082; PubMed=9266104;
RA Shaw-Bruha C.M., Pirruccello S.J., Shull J.D.;
RT "Expression of the prolactin gene in normal and neoplastic human
RL breast tissues and human mammary cell lines: promoter usage and
RT alternative mRNA splicing." ;
RN Breast Cancer Res. Treat. 44:243-253(1997).
[7]
RP SEQUENCE OF 29-227.
RX MEDLINE=78046207; PubMed=925136;
RA Shome B., Parlow A.F.;
RT "Human pituitary prolactin (hPRL): the entire linear amino acid
RL sequence." ;
RN J. Clin. Endocrinol. Metab. 45:1112-1115(1977).
[8]
RP SEQUENCE OF 29-53.
RX MEDLINE=75151509; PubMed=1126929;
RA Jacobs J.W., Niall H.D.;
RT "High sensitivity automated sequence determination of polypeptides." ;
RL J. Biol. Chem. 250:3629-3636(1975).
CC -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC promoting lactation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 8.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X00540; CAA25214.1; -
DR EMBL; X00541; CAA25214.1; JOINED.
DR EMBL; X00543; CAA25214.1; JOINED.
DR EMBL; X00544; CAA25214.1; JOINED.
DR EMBL; V00566; CAA23829.1; -
DR EMBL; X54393; CAA38263.1; ALT FRAME.
DR EMBL; X54393; CAA38264.1; ALT FRAME.
DR EMBL; BC015850; AAH15850.1; -
DR EMBL; M29386; AAA60173.1; -
DR EMBL; D00411; BAA00312.1; -
DR EMBL; U75583; AAB70858.1; -
DR PIR; A90998; LCHU.
DR HSSP; Q28632; LAN3.
DR Genew; HGNC:9445; PRL.
DR MIM; 176760; -
DR GO; GO:0005148; P:prolactin receptor binding; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0007516; P:hemocyt development; TAS.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone. 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN 1; 1.
DR PROSITE; PS00338; SOMATOTROPIN 2; 1.
DR Hormone; Lactation; Pituitary; Signal; Glycoprotein.
FT SIGNAL 1 28
DR CHAIN 29 227 PROLACTIN.
```

```
FT DISULFID 32 39 BY SIMILARITY.
FT DISULFID 86 202 BY SIMILARITY.
FT DISULFID 219 227 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC... ) (PARTIAL).
FT CONFLICT 42 42 T -> A (IN REF. 6).
FT CONFLICT 110 111 SL -> VS (IN REF. 6).
FT CONFLICT 113 114 VS -> L (IN REF. 7).
FT CONFLICT 118 118 S -> P (IN REF. 6).
FT CONFLICT 148 148 E -> Q (IN REF. 5).
FT CONFLICT 172 172 N -> D (IN REF. 7).
FT CONFLICT 190 191 ES -> SE (IN REF. 7).
FT CONFLICT 206 206 D -> H (IN REF. 5).
FT SEQUENCE 227 AA; 25876 MW; 952BBA1B6A955527 CRC64;

Query Match 100.0%; Score 1043; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.6e-77;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGGAARCVTLRDLFDRAVVLSHYIHLNLSSEMFEDKRYTHGRGITKAINSCHT 60
Db 29 LPICPGGAARCVTLRDLFDRAVVLSHYIHLNLSSEMFEDKRYTHGRGITKAINSCHT 88
QY 61 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQAPAILSKAVEIE 120
Db 89 SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLYHLVTEVRGMQAPAILSKAVEIE 148
QY 121 EQTKRLLEGMLIVSQVHPETKENIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRD 180
Db 149 EQTKRLLEGMLIVSQVHPETKENIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRD 208
QY 181 KIDNYLKLLKCRILHNHNC 199
Db 209 KIDNYLKLLKCRILHNHNC 227

RESULT 2
PRL_MACMU
ID PRL_MACMU STANDARD; PRT; 227 AA.
AC P55151;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolactin precursor (PRL).
GN PRL.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Decidua;
RX MEDLINE=94220570; PubMed=8167226;
RA Brown N.A., Betha C.L.;
RT "Cloning of decidal prolactin from rhesus macaque." ;
RL Biol. Reprod. 50:543-552(1994).
CC -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC promoting lactation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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DR EMBL; U09018; AAA18471.1; -
DR HSSP; Q28632; LAN3.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
```



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Db 61 SSLPTPEDKEQAQINQKOPLSIVLSIRSWNEPLVHLVTEVRGMEAPAILSKAVEIE 120
QY 121 EQTKRLLEGMLIVSOVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSE 180
Db 121 EQTKRLLEGMLIVSOVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSE 180
QY 181 KIDNYLKLLKCRITIHNNNC 199
Db 181 KIDNYLKLLKCRITIHNNNC 199

RESULT 2
Q8HXS1 PRELIMINARY; PRT; 229 AA.
AC Q8HXS1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Prolactin precursor.
OS Ailuropoda melanoleuca (Giant panda).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ailuropoda.
OX NCBI_TaxID=9646;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Pituitary;
RA Zheng X., Zhu M., Zhang Z.;
RT "Cloning and expression of pituitary prolactin gene in Ailuropoda melanoleuca";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161285; AAN78320.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 229 AA; 26236 MW; 441E3D748CFDDBC2 CRC64;
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Query Match 84.2%; Score 878; DB 6; Length 229;
Best Local Similarity 79.9%; Pred. No. 1.3e-69;
Matches 159; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEDFKRYTHGRGFTTKAINSCHT 60
Db 31 LPICPTGAVNCQVSLRDLFDRAVLVSHYIHLNLSSEMFSEDFKRYAQGRGFTTKAINSCHT 90
QY 61 SSLATPEDKEQAQNMOKDFLSIVLSIRSWNEPLVHLVTEVRGMEAPAILSKAVEIE 120
Db 91 SSLSTPEDKEQAQIHHEDLLNLVLSRWNPLVHLVTEVRGMEAPDSILSRATEIE 150
QY 121 EQTKRLLEGMLIVSOVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSE 180
Db 151 EQNRRLLEGMEKIVGQVHPGVRENEVSVWSGLPSLQMADEESRLFAFYNLLHCLRRDSE 210
QY 181 KIDNYLKLLKCRITIHNNNC 199
Db 211 KIDNYLKLLKCRIVYDSNC 229

Query Match 84.1%; Score 877; DB 6; Length 229;
Best Local Similarity 79.9%; Pred. No. 1.5e-69;
Matches 159; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

QY 1 LPICPGGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEDFKRYTHGRGFTTKAINSCHT 60
Db 31 LPICPTGAVNCQVSLRDLFDRAVLVSHYIHLNLSSEMFSEDFKRYAQGRGFTTKAINSCHT 90
QY 61 SSLATPEDKEQAQNMOKDFLSIVLSIRSWNEPLVHLVTEVRGMEAPAILSKAVEIE 120
Db 91 SSLSTPEDKEQAQIHHEDLLNLVLSRWNPLVHLVTEVRGMEAPDSILSRATEIE 150
QY 121 EQTKRLLEGMLIVSOVHPETKENEIYPVWSGLPSLQMADEESRLSAYNLLHCLRRDSE 180
Db 151 EQNRRLLEGMEKIVGQVHPGVRENEVSVWSGLPSLQMADEESRLFAFYNLLHCLRRDSE 210
QY 181 KIDNYLKLLKCRITIHNNNC 199
Db 211 KIDNYLKLLKCRIVYDSNC 229

RESULT 4
Q8T110 PRELIMINARY; PRT; 222 AA.
AC Q8T110;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Prolactin precursor (Fragment).
GN PRL.
OS Taenia hydatigena.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_TaxID=85431;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Z.;
RT "Cloning and analysis of the prolactin of cestode.";
EL Chin. J. Vet. Sci. 22:157-159(2002).
DR EMBL; AJ457817; CAD30063.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT NON_TER 1 1
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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:12:18 ; Search time 32 Seconds
(without alignments)
321.049 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 1043

Sequence: 1 LPIPCGAGRCQVLRDLFD.....HKIDNYLKLLKCRIRHNNNC 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1043	100.0	199	3	US-08-737-248-7
2	1043	100.0	351	1	US-08-196-350-1
3	887	85.0	199	3	US-08-737-248-10
4	877	84.1	199	3	US-08-737-248-12
5	876	84.0	199	3	US-08-737-248-8
6	871	83.5	199	3	US-08-737-248-14
7	797	76.4	199	3	US-08-737-248-13
8	796	76.3	199	3	US-08-737-248-11
9	786.5	75.4	198	3	US-08-737-248-6
10	754	72.3	199	3	US-08-737-248-2
11	754	72.3	426	3	US-08-737-248-4
12	748	71.7	199	3	US-08-737-248-5
13	737	70.7	199	3	US-08-737-248-9
14	667	64.0	197	3	US-08-737-248-15
15	667	64.0	197	3	US-08-737-248-17
16	630	60.4	125	3	US-08-985-526-25
17	630	60.4	253	3	US-08-985-526-27
18	621	59.5	197	3	US-08-737-248-16
19	370	35.5	199	3	US-08-737-248-23
20	280	26.8	187	3	US-08-737-248-18
21	280	26.8	187	3	US-08-737-248-19
22	270	25.9	177	3	US-08-737-248-21
23	269.5	25.8	188	3	US-08-737-248-20
24	263	25.2	236	3	US-09-602-848-2
25	245	23.5	223	3	US-09-602-848-4
26	210.5	20.2	207	1	US-07-656-566-2
27	210.5	20.2	231	1	US-07-656-566-3

28 206 19.8 191 3 US-08-737-248-22 Sequence 22, Appli
29 192 18.4 191 1 US-08-093-383-3 Sequence 3, Appli
30 192 18.4 217 3 US-08-589-028-10 Sequence 10, Appli
31 192 18.4 217 3 US-08-784-582-10 Sequence 10, Appli
32 192 18.4 217 3 US-08-785-271-10 Sequence 10, Appli
33 192 18.4 217 3 US-08-759-628-11 Sequence 11, Appli
34 192 18.4 217 4 US-09-284-878-1 Sequence 1, Appli
35 192 18.4 217 4 US-09-511-024A-1 Sequence 1, Appli
36 190 18.2 191 1 US-07-885-689A-29 Sequence 23, Appli
37 190 18.2 191 4 US-09-539-746-2 Sequence 2, Appli
38 190 18.2 193 2 US-08-383-621-2 Sequence 2, Appli
39 190 18.2 193 3 US-08-459-906-2 Sequence 2, Appli
40 190 18.2 199 1 US-07-801-164A-4 Sequence 4, Appli
41 190 18.2 217 2 US-09-105-651-2 Sequence 2, Appli
42 189 18.1 191 4 US-09-511-024A-9 Sequence 9, Appli
43 189 18.1 217 1 US-08-469-486-51 Sequence 51, Appli
44 189 18.1 217 2 US-08-469-658-51 Sequence 51, Appli
45 185 17.7 191 4 US-09-511-024A-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-737-248-7
; Sequence 7, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
; APPLICANT: Guemene, Daniel
; APPLICANT: Zadworny, David
; APPLICANT: Karatzas, Costas
; TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
; TITLE OF INVENTION: TREATING BIRD BROODNESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,248
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR95/00576
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/05550
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6411P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-737-248-7

Query Match 100.0%; Score 1043; DB 3; Length 199;

Best Local Similarity 100.0%; Pred. No. 3.7e-98; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 1 LPTCPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
Db 1 LPTCPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60

QY 61 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 61 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

QY 121 EQTKRLLGEMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRDSDH 180
Db 121 EQTKRLLGEMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRDSDH 180

QY 181 KIDNYLKLKCRILHNHNC 199
Db 181 KIDNYLKLKCRILHNHNC 199

RESULT 2
US-08-196-350-1
; Sequence 1, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Mosciaki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brad Salcedo
; STREET: One Kendall Square
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/196,350
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gosz, William G
; REGISTRATION NUMBER: 27,787
; REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 6172527868
; TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human prolactin
; US-08-196-350-1

Query Match 100.0%; Score 1043; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 8.1e-98; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 1 LPTCPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
Db 153 LPTCPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 212

QY 61 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 213 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 272

QY 121 EQTKRLLGEMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRDSDH 180
Db 273 EQTKRLLGEMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRDSDH 332

QY 181 KIDNYLKLKCRILHNHNC 199
Db 333 KIDNYLKLKCRILHNHNC 351

RESULT 3
US-08-737-248-10
; Sequence 10, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
; APPLICANT: Guemene, Daniel
; APPLICANT: Zadworny, David
; APPLICANT: Karatzas, Costas
; TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
; TITLE OF INVENTION: TREATING BIRD BROODINESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,248
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR95/00576
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/05550
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6411P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-737-248-10

Query Match 85.0%; Score 887; DB 3; Length 199;
Best Local Similarity 81.4%; Pred. No. 2.6e-82; Indels 0; Gaps 0;
Matches 162; Conservative 22; Mismatches 15;

QY 1 LPICPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
Db 1 LPICPGAARCOVTLRDLFDRAVLVSHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60

QY 61 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
Db 61 SSLATPEDKEAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:16:44 ; Search time 123 Seconds
(without alignments)

457.130 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199

Sequence: 1 LPICPGAARQVTLRLDFD.....HKIDNYLKLRKRIHNNC 199

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	100.0	199	2	AAY31764 Human pro
2	199	100.0	199	5	ABG94847 Human pro
3	199	100.0	200	2	Aaw92258 Human ant
4	199	100.0	227	2	Aar05231 AA sequen
5	199	100.0	227	4	AAG78336 Human pro
6	199	100.0	227	4	AAG78336 Human pro
7	199	100.0	227	7	AD48810 Human pro
8	199	100.0	351	2	Aar78691 Prolactin
9	185	93.0	359	2	AAR05805
10	178	89.4	228	2	Aaw23626 Prolactin
11	178	89.4	228	2	Aaw23626 Prolactin
12	136	68.3	173	6	AA016662 Human ext
13	128	64.3	227	4	AAG78337 Mutant hu
14	124	62.3	125	2	AAW40299 Human pro
15	124	62.3	227	1	AAPE2079 Human pre
16	124	62.3	252	2	Aaw40300 Human con
17	111	55.8	199	6	ABU09878 Human pro
18	111	55.8	199	6	ABU09846 Human pro
19	103	51.8	199	2	AAW23629 Human pro
20	101	50.8	199	3	AAW78428 Human pro
21	81	40.7	140	2	AAW92260 Human ant
22	81	40.7	143	2	AAW92261 Human ant
23	76	38.2	167	6	AA016658 Human ext
24	68	34.2	125	2	AAW06194 Anti-angi
25	68	34.2	253	2	AAW06195 Anti-angi

ALIGNMENTS

RESULT 1

AAAY31764	124	2	AAW92259	Human ant
ID	AAAY31764 standard; protein; 199 AA.			
XX				
AC	AAAY31764;			
XX	*			
DT	06-DEC-1999 (first entry)			
XX				
DE	Human prolactin.			
XX				
KW	Prolactin; human; variant; protein engineering.			
XX				
OS	Homo sapiens.			
XX				
FH	Key			
FT	Misc-difference 59			
FT	/note= "optionally substituted by Phe in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 60			
FT	/note= "optionally substituted by Ser in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 61			
FT	/note= "optionally substituted by Glu in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 63			
FT	/note= "optionally substituted by Ile in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 64			
FT	/note= "optionally substituted by Pro in human prolactin variant of Claim 8"			
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FT	/note= "optionally substituted by Ser in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 68			
FT	/note= "optionally substituted by Asn in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 69			
FT	/note= "optionally substituted by Arg in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 71			
FT	/note= "optionally substituted by Glu in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 72			
FT	/note= "optionally substituted by Thr in human prolactin variant of Claim 8"			
FT				
FT	Misc-difference 75			
FT	/note= "optionally substituted by Lys in human prolactin variant of Claim 8"			
FT				

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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:25:35 ; Search time 40 Seconds
(without alignments)
478.553 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 199
Sequence: 1 LPICPGARQCQTLDLFD.....HKIDNYLKLLKCRILHNNNC 199

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	100.0	227	1 LCHU	prolactin precursor
2	195	98.0	228	2 A61402	prolactin precursor
3	26	13.1	199	2 S15131	prolactin - Arabia
4	26	13.1	229	1 LCPG	prolactin - Arabia
5	25	12.6	175	2 S18882	prolactin - Americ
6	25	12.6	199	1 LCHO	prolactin - horse
7	24	12.1	134	2 I51233	prolactin - Japane
8	24	12.1	198	1 A60620	prolactin - Green
9	24	12.1	207	2 A60969	prolactin precursor
10	19	9.5	229	2 A61133	prolactin precursor
11	19	9.5	229	2 A60972	prolactin precursor
12	17	8.5	229	2 JC4631	prolactin precursor
13	16	8.0	199	2 PN0128	prolactin - sei wh
14	14	7.0	226	1 LCRT	prolactin precursor
15	13	6.5	228	1 LCMS	prolactin precursor
16	12	6.0	229	1 LCBO	prolactin precursor
17	12	6.0	229	1 LCSH	prolactin precursor
18	12	6.0	229	2 I83982	prolactin - goat
19	10	5.0	198	2 B28106	prolactin, 24K - M
20	10	5.0	199	2 JS0430	prolactin - elepha
21	10	5.0	212	2 A32477	prolactin I precu
22	10	5.0	212	2 I51034	prolactin-I - Moza
23	9	4.5	200	2 S34604	prolactin - marble
24	9	4.5	209	2 S30541	prolactin precursor
25	8	4.0	177	2 A28106	prolactin, 20K - M
26	8	4.0	187	2 S06677	prolactin II - chu
27	8	4.0	187	2 S02304	prolactin II - chu
28	8	4.0	200	2 B32477	prolactin II precu
29	8	4.0	207	2 S21965	prolactin - silver

RESULT 1
LCHU

prolactin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1979 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000

C:Accession: A90998; A92318; A28867; PNO089; A92762; A92177; A01505

R:Truong, A.T.; Duez, C.; Belayew, A.; Renard, A.; Pictet, R.; Bell, G.I.; Martial, J.A.

EMBO J. 3, 429-437, 1984

A:Title: Isolation and characterization of the human prolactin gene.

A:Reference number: A90998; MUID:84182507; PMID:6325171

A:Accession: A90998

A:Molecule type: DNA

A:Residues: 1-227 <TRU>

R:Cooke, N.E.; Coit, D.; Shine, J.; Baxter, J.D.; Martial, J.A.

J. Biol. Chem. 256, 4007-4016, 1981

A:Title: Human prolactin: cDNA structural analysis and evolutionary comparisons.

A:Reference number: A92318; MUID:81168179; PMID:6260780

A:Accession: A92318

A:Molecule type: mRNA

A:Residues: 1-227 <COO>

A:Cross-references: GB:V00566; GB:J00299; NID:g34210; PIDN:CAA23829.1; PID:g34211

R:Takahashi, H.; Nabeshima, Y.; Nabeshima, Y.; Ogata, K.; Takeuchi, S.

J. Biochem. 95, 1491-1499, 1984

A:Title: Molecular cloning and nucleotide sequence of DNA complementary to human decidua

A:Reference number: A28867; MUID:84264464; PMID:6146607

A:Accession: A28867

A:Molecule type: mRNA

A:Residues: 1-205, 'H' 207-227 <TAK>

A:Cross-references: EMBL:M29386

A:Note: The authors translated the codon CAT for residue 206 as Asp

R:Merzvetsov, N.P.; Golovin, S.Y.; Zelenin, S.M.; Morozova, T.Y.; Karginov, V.A.; Chekhr

Biorg. Khim. 13, 1687-1690, 1987

A:Title: Synthesis, cloning and sequencing of cDNA complementary to mRNA of prolactin fr

A:Reference number: PNO089; MUID:88221681; PMID:3450284

A:Accession: PNO089

A:Molecule type: mRNA

A:Residues: 45-227 <MER>

A:Experimental source: pituitary gland

A:Note: The authors translated the codon AAC for residue 15 as Asp

R:Shone, B.; Parlow, A.F.

J. Clin. Endocrinol. Metab. 45, 1112-1115, 1977

A:Title: Human pituitary prolactin (hPRL): the entire linear amino acid sequence.

A:Reference number: A92762; MUID:78046207; PMID:925136

A:Accession: A92762

A:Molecule type: protein

A:Residues: 29-109, 'VS', 112, 'L', 115-132, 'X', 134-171, 'D', 173-189, 'SE', 192-227 <SHO>

R:Jacobs, J.W.; Niall, H.D.

J. Biol. Chem. 250, 3629-3636, 1975

A:Title: High sensitivity automated sequence determination of polypeptides.

A:Reference number: A92177; MUID:75151509; PMID:1126929

A:Accession: A92177

A:Molecule type: protein

A;Residues: 29-52,'L' <JAC> C;Genetics: A;Gene: GDB:PRL A;Cross-references: GDB:119517; OMIM:176760 A;Map position: 6p22.2-6p22.1 C;Introns: 9/3; 68/3; 104/3; 164/3 A;Superfamily: prolactin C;Keywords: anterior pituitary; hormone; lactation; placenta F;1-28/Domain: signal sequence #status predicted <SIG> F;29-227/Product: prolactin #status experimental <MAT> F;32-39,86-202,219-227/Disulfide bonds: #status predicted		Query Match 100.0%; Score 199; DB 1; Length 227; Best Local Similarity 100.0%; Pred. No. 2.3e-201; Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 LPICPGGARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 60 	Db	29 LPICPGGARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHT 88
Qy	61 SSLATPEDEKQAQMNQKQFSLIVSLRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 120 	Db	89 SSLATPEDEKQAQMNQKQFSLIVSLRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 148
Qy	121 EQTKRLLEGMLIVSQVHPETKENIYPVWGLPSLQMADEESRLSAYYNLHCLRDSDH 180 	Db	149 EQTKRLLEGMLIVSQVHPETKENIYPVWGLPSLQMADEESRLSAYYNLHCLRDSDH 208
Qy	181 KIDNYLKLCRIIHNNC 199 	Db	209 KIDNYLKLCRIIHNNC 227
RESULT 2			
A61402			
prolactin precursor, placental (clone 204) - human			
C;Species: Homo sapiens (man) C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Feb-1997 C;Accession: A61402 R;Hiraoka, Y.; Tatsumi, K.; Shiozawa, M.; Aiso, S.; Fukasawa, T.; Yasuda, K.; Miyai, K. Mol. Cell. Endocrinol. 75, 71-80, 1991 A;Title: A placenta-specific 5' non-coding exon of human prolactin. A;Reference number: A61402; MUID:91267286; PMID:2050267 A;Accession: A61402 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-228 <HIR> C;Superfamily: prolactin C;Keywords: alternative splicing F;87-203,220-228/Disulfide bonds: #status predicted			
Query Match 98.0%; Score 195; DB 2; Length 228; Best Local Similarity 100.0%; Pred. No. 3.8e-197; Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	5 PGGAARQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHTSLA 64 	Db	34 PGGAARQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFTTKAINSCHTSLA 93
Qy	65 TPEDKEQAQMNQKQFSLIVSLRSWNEPLYHLVTEVRGMOEAPAILSKAVEIEQTK 124 	Db	94 TPEDKEQAQMNQKQFSLIVSLRSWNEPLYHLVTEVRGMOEAPAILSKAVEIEQTK 153
Qy	125 RLLEGMLIVSQVHPETKENIYPVWGLPSLQMADEESRLSAYYNLHCLRRDSHKIDN 184 	Db	154 RLLEGMLIVSQVHPETKENIYPVWGLPSLQMADEESRLSAYYNLHCLRRDSHKIDN 213
Qy	185 YLKLLKCRIIHNNC 199 	Db	214 YLKLLKCRIIHNNC 228
RESULT 3			
prolactin precursor - pig			
C;Species: Sus scrofa domestica (domestic pig) C;Date: 24-Apr-1984 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999 C;Accession: S04077; A60971; A01507 R;Schulz-Aellen, M.F.; Schmid, E.; Movva, R.N. Nucleic Acids Res. 17, 3295, 1989 A;Title: Nucleotide sequence of porcine preprolactin cDNA. A;Reference number: S04077; MUID:89263739; PMID:2726463 A;Accession: S04077 A;Molecule type: mRNA A;Residues: 1-229 <SCH> A;Cross-references: EMBL:X14068; NID:g2082; PIDN:CAA32231.1; PID:g2083 R;Kato, Y.; Hirai, T.; Kato, T. J. Mol. Endocrinol. 4, 135-142, 1990 A;Title: Molecular cloning of cDNA for porcine prolactin precursor. A;Reference number: A60971; MUID:90262633; PMID:2344390 A;Accession: A60971 A;Molecule type: mRNA A;Residues: 1-3,'R','5','X','7-42','V','44-229 <KAT> R;Li, C.H. Int. J. Pept. Protein Res. 8, 205-224, 1976 A;Title: Studies on pituitary lactogenic hormone. The primary structure of the porcine A;Reference number: A91770; MUID:76189476; PMID:1270193 A;Accession: A01507 A;Molecule type: protein A;Residues: 31-42,'V','44-151','B','153-225','N',227-229 <LIC> C;Superfamily: prolactin C;Keywords: anterior pituitary; hormone; lactation; placenta F;1-30/Domain: signal sequence #status predicted <SIG> F;33-229/Product: prolactin #status experimental <MAT> F;34-41,88-204,221-229/Disulfide bonds: #status experimental			
Query Match 13.1%; Score 26; DB 1; Length 229; Best Local Similarity 100.0%; Pred. No. 2.7e-19; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	169 YNLLHCLRRDSHKIDNYLKLCRII 194 	Db	199 YNLLHCLRRDSHKIDNYLKLCRII 224

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:17:24 ; Search time 24 Seconds
(without alignments)

431.748 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199

Sequence: 1 LPICFGGAQCQVTLRLDLPD.....HKIDNYLKLKRIHNNNC 199

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	100.0	227	1 PRL_HUMAN	P01236 homo sapien
2	52	26.1	227	1 PRL_MACMU	P55151 macaca mula
3	26	13.1	199	1 PRL_CANDR	P22393 camelus dro
4	26	13.1	227	1 PRL_RABIT	Q28632 oryctolagus
5	26	13.1	229	1 PRL_PIG	P01238 sus scrofa
6	25	12.6	193	1 PRL_MUSVI	P29234 mustela vis
7	25	12.6	199	1 PRL_HORSE	P12420 equus cabal
8	24	12.1	134	1 PRL_BURJA	P43001 bufo japoni
9	24	12.1	198	1 PRL_CHEMY	P33090 cheloniamy
10	24	12.1	228	1 PRL_MONDO	O62819 monodelphis
11	24	12.1	228	1 PRL_TRIVU	O62781 trichosurus
12	19	9.5	229	1 PRL_CHICK	P14676 gallus gall
13	19	9.5	229	1 PRL_MELGA	P17572 meleagris g
14	17	8.5	199	1 PRL1_ALLMI	P55751 alligator m
15	17	8.5	199	1 PRL1_CRONO	P55753 crocodylus
16	17	8.5	199	1 PRL2_ALLMI	P55752 alligator m
17	17	8.5	199	1 PRL2_CRONO	P55754 crocodylus
18	17	8.5	229	1 PRL_FELCA	P46403 felis silve
19	16	8.0	199	1 PRL_BALBO	P33089 balaeopter
20	14	7.0	226	1 PRL_RAT	P01237 rattus norv
21	13	6.5	226	1 PRL_MOUSE	P06879 mus musculu
22	12	6.0	229	1 PRL_BOVIN	P01239 bos taurus
23	12	6.0	229	1 PRL_CAPHI	Q2818 capra hircu
24	12	6.0	229	1 PRL_SHEEP	P01240 ovis aries
25	10	5.0	199	1 PRL1_LOXAF	P10765 loxodonta a
26	10	5.0	212	1 PRL1_OREMO	P09319 oreochromis
27	9	4.5	209	1 PRL1_PROAT	P33091 proteotermis
28	9	4.5	209	1 PRL2_ANGAN	P33096 anguilla an
29	8	4.0	200	1 PRL2_OREMO	P09318 oreochromis
30	8	4.0	207	1 PRL1_HYPMO	P35395 hypophthalm
31	8	4.0	210	1 PRL2_ONCKE	P09584 oncorhynch
32	8	4.0	210	1 PRL2_ONCTS	Q91364 oncorhynch
33	8	4.0	210	1 PRL2_CARAU	P87495 carassius a

34	8	4.0	210	1 PRL_CORAU	P34181 coregonus a
35	8	4.0	210	1 PRL_CYPCA	P09585 cyprinus ca
36	8	4.0	210	1 PRL_HYPNO	P29235 hypophthalm
37	8	4.0	210	1 PRL_ONCMY	P21993 oncorhynch
38	8	4.0	210	1 PRL_SALSA	P48096 salmo salar
39	8	4.0	211	1 PRL1_ONCKE	P09583 oncorhynch
40	8	4.0	211	1 PRL1_PAROL	Q9YGV6 paralichthy
41	8	4.0	212	1 PRL1_DICLA	P48249 dicentrarch
42	8	4.0	212	1 PRL1_ICIPU	P51904 ictalurus p
43	8	4.0	212	1 PRL1_SPAAU	O93337 sparus aura
44	8	4.0	226	1 PRL1_MESAU	P37884 mesocricetu
45	8	4.0	227	1 PRL1_RAT	P09320 rattus norv

ALIGNMENTS

RESULT 1

PRL_HUMAN	STANDARD;	PRT;	227 AA.
AC	P01236; Q15199; Q92996;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Prolactin precursor (PRL).		
GN	PRL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84182507; PubMed=6325171;		
RA	Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,		
RA	Martial J.A.;		
RT	"Isolation and characterization of the human prolactin gene.";		
RL	EMBO J. 3:429-437(1984).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=81168179; PubMed=6260780;		
RA	Cooke N.E., Coit D., Shine J., Baxter J.D., Martial J.A.;		
RT	"Human prolactin. cDNA structural analysis and evolutionary		
RT	comparisons.";		
RL	J. Biol. Chem. 256:4007-4016 (1981).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91267286; PubMed=2050267;		
RA	Hiraka Y., Tatsumi K., Shiozawa M., Aiso S., Fukasawa T., Yasuda K.,		
RA	Miyai K.;		
RT	"A placenta-specific 5' non-coding exon of human prolactin.";		
RL	Mol. Cell. Endocrinol. 75:71-80(1990).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,		
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		

FT	DISULFID	32	39	BY SIMILARITY.
FT	DISULFID	86	202	BY SIMILARITY.
FT	DISULFID	219	227	BY SIMILARITY.
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (PARTIAL).
FT	CONFLICT	42	42	T -> A (IN REF. 6).
FT	CONFLICT	110	111	SL -> VS (IN REF. 7).
FT	CONFLICT	113	114	VS -> L (IN REF. 7).
FT	CONFLICT	118	118	S -> P (IN REF. 6).
FT	CONFLICT	148	148	E -> Q (IN REF. 5).
FT	CONFLICT	172	172	N -> D (IN REF. 7).
FT	CONFLICT	190	191	ES -> SE (IN REF. 7).
FT	CONFLICT	206	206	D -> H (IN REF. 5).
FT	SEQUENCE	227 AA;	25876 MW;	952BBA1B6A95527 CRC64;
Query Match		100.0%;	Score 199;	DB 1; Length 227;
Best Local Similarity		100.0%;	Pred. No. 2.3e-203;	
Matches 199;	Conservative	0;	Mismatches	0; Indels
QY	1	LPICPGGAARCVTLIEDLFDRAVVLVSHYIHNLSSEMFSEFDKRYTHGRGFTKAINSCHT	60	
DB	29	LPICPGGAARCVTLIEDLFDRAVVLVSHYIHNLSSEMFSEFDKRYTHGRGFTKAINSCHT	88	
QY	61	SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE	120	
DB	89	SSLATPEDKEQAQOMNQKDFLSLIVSLRSWNEPLVHLVTEVRGMQEAPEAILSKAVEIE	148	
QY	121	EQTKRLLLEGMEILVSVQHPETKENEIYPVWVGPSIQMADEESRLSAYNLLHCLRRDHS	180	
DB	149	EQTKRLLLEGMEILVSVQHPETKENEIYPVWVGPSIQMADEESRLSAYNLLHCLRRDHS	208	
QY	181	KIDNYLKLKCRIIHNHNC	199	
DB	209	KIDNYLKLKCRIIHNHNC	227	
RESULT 2				
PRL MACMU		STANDARD;	PRT;	227 AA.
ID	PRL MACMU			
AC	P55151;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Prolactin precursor (PRL).			
GN	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9544;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Decidua;			
EX	MEDLINE=94220570; PubMed=6167226;			
EA	Brown N.A.; Bethea C.L.;			
RL	"Cloning of decidua prolactin from rhesus macaque.";			
RT	Biol. Reprod. 50:543-552(1994).			
CC	!- FUNCTION: Prolactin acts primarily on the mammary gland by			
CC	promoting lactation.			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- SIMILARITY: Belongs to the somatotropin/prolactin family.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce			
CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; U09018; AAA18471.1; -.			
DR	HSSP; Q28632; 1AN3.			
DR	InterPro; IPR001400; Somatotropin.			
DR	Pfam; PF00103; hormone; 1.			

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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:24:30 ; Search time 117 Seconds
(without alignments)
536.651 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199

Sequence: 1 LPICPGAACRCQVTLRDLED.....HKIDNYLKLLKCRILHNHNC 199

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	22.1	199	6	Q9TS41
2	35	17.6	44	4	Q9UD31
3	29	14.6	222	5	Q8T110
4	25	12.6	229	6	Q8HXS1
5	25	12.6	229	6	Q864R8
6	24	12.1	214	13	Q8JFX6
7	23	11.6	233	13	Q7T1A5
8	16	8.0	16	4	Q9UP51
9	14	7.0	161	11	Q63293
10	13	6.5	225	11	Q9CPQ0
11	13	6.5	225	11	Q9CYL2
12	13	6.5	226	11	Q9CYL8
13	13	6.5	228	11	Q9CPQ2
14	12	6.0	103	13	Q9PSP9
15	12	6.0	103	13	Q9PSP8
16	12	6.0	229	13	Q90ZB1

Q9QZL1 microtus mo
Q9PWF9 coturnix co
Q7ZV3 anguilla ja
Q9R0S8 rattus norv
Q8K3W4 rattus norv
Q9PWQ4 gallus gall
Q805E3 periophthal
Q91170 oncorhynch
Q801K3 brachydanic
Q7T1A8 perca flave
Q90ZN5 heteropneus
Q7ZZM0 sparus aua
Q3Z56 mus musculu
Q8CJ42 rattus norv
Q44166 caenorhabdi
Q56591 vibrio angu
Q8Z0A9 anabaena sp
Q8G183 bruceella su
Q89YK7 bacteroides
Q7XWS5 oryza sativ
Q43161 homo sapien
Q9UP51 homo sapien
Q88778 rattus norv
Q8737 mus musculu
Q9JJM8 rattus norv
Q9T18 macropus ru
Q9VE38 drosophila
Q87T17 vibrio para
Q9I889 oncorhynch

ALIGNMENTS

RESULT 1

Q9TS41
ID Q9TS41 PRELIMINARY; PRT; 199 AA.
AC Q9TS41;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Prolactin.
OS Papio (baboons).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae.
OX NCBI_TaxID=9554;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92037387; PubMed=1935793;
RA Cole E.S., Nichols E.H., Lauziere K., Edmunds T., McPherson J.M.;
RT "Characterization of the microheterogeneity of recombinant primate
RT prolactin: implications for posttranslational modifications of the
RT hormone in vivo."
RL Endocrinology 129:2639-2646(1991).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00286; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 199 AA; 22850 MW; 872A8935FEA43B67 CRC64;

Query Match 22.1%; Score 44; DB 6; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.9e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 EPEALLSKAVEIEETQKLEGMELIVSQVHPETKENIYPW 150
|||||
DB 107 EPEALLSKAVEIEETQKLEGMELIVSQVHPETKENIYPW 150

Db	63 KRYTHGRGFTTKAINSCHTSSLATPEDKE 91		
RESULT 4			
Q8HXS1	PRELIMINARY;	PRT;	229 AA.
ID	Q8HXS1		
AC	Q8HXS1;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Prolactin precursor.		
OS	Ailuropoda melanoleuca (Giant panda).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ailuropoda.		
OX	NCBI_TaxID=9646;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pituitary;		
RA	Zheng X., Zhu M., Zhang Z.;		
RT	"Cloning and expression of pituitary prolactin gene in Ailuropoda		
RL	melanoleuca.";		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AY161285; AAN78320.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00103; hormone; 1.		
DR	PRINTS; PR00836; SOMATOTROPIN.		
DR	PROSITE; PS00266; SOMATOTROPIN_1; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
KW	Signal.		
FT	SIGNAL	1	30
SQ	SEQUENCE 229 AA; 26236 MW; 441E3D748CFDDBC2 CRC64;		
Query Match 12.6%; Score 25; DB 6; Length 229;			
Best Local Similarity 100.0%; Pred. No. 2.3e-17;			
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	169 YNLHCLRRDSHKIDNYLKLLKRI 193		
Db	199 YNLHCLRRDSHKIDNYLKLLKRI 223		
RESULT 5			
Q864R8	PRELIMINARY;	PRT;	229 AA.
ID	Q864R8		
AC	Q864R8;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Preprolactin precursor.		
OS	Mustela vison (American mink).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;		
OX	NCBI_TaxID=9667;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Vardy T.L., Farid A.;		
RT	"Nucleotide sequence variation of the mink preprolactin gene.";		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY249860; AAO92934.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00103; hormone; 1.		
DR	PRINTS; PR00836; SOMATOTROPIN.		
DR	PROSITE; PS00266; SOMATOTROPIN_1; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
KW	Signal.		
FT	SIGNAL	1	30
FT	CHAIN	31	70
FT	CHAIN	71	106

Db	42 KRYTHGRGFTTKAINSCHTSSLATPEDKE 70		
RESULT 2			
Q9UDA3	PRELIMINARY;	PRT;	44 AA.
ID	Q9UDA3		
AC	Q9UDA3;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Prolactin (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
MD	MEDLINE=93292510; PubMed=8513798;		
RA	Goffin V., Struman I., Goormaghtigh E., Martial J.A.;		
RT	"The addition of nine residues at the C-terminus of human prolactin		
RT	drastically alters its biological properties.";		
RL	Eur. J. Biochem. 214:483-490(1993).		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00103; hormone; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
SQ	SEQUENCE 44 AA; 5416 MW; 707E91C66398F4BF CRC64;		
Query Match 17.6%; Score 35; DB 4; Length 44;			
Best Local Similarity 100.0%; Pred. No. 2.4e-28;			
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	165 LSAYNLLHCLRRDSHKIDNYLKLLKRIIHNNC 199		
Db	1 LSAYNLLHCLRRDSHKIDNYLKLLKRIIHNNC 35		
RESULT 3			
Q8T110	PRELIMINARY;	PRT;	222 AA.
ID	Q8T110		
AC	Q8T110;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Prolactin precursor (Fragment).		
GN	PRL.		
OS	Taenia hydatigena.		
OC	Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;		
OC	Cyclophyllidae; Taeniidae; Taenia.		
OX	NCBI_TaxID=85431;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chen Z.;		
RT	"Cloning and analysis of the prolactin of cestode.";		
RL	Chin. J. Vet. Sci. 22:157-159(2002).		
DR	EMBL; AJ457817; CAD30063.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00103; hormone; 1.		
DR	PRINTS; PR00836; SOMATOTROPIN.		
DR	PROSITE; PS00266; SOMATOTROPIN_1; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
KW	Signal.		
FT	NON TER	1	1
FT	SIGNAL	<1	22
FT	CHAIN	23	222
SQ	SEQUENCE 222 AA; 25346 MW; 310BFAF18799EF332 CRC64;		
Query Match 14.6%; Score 29; DB 5; Length 222;			
Best Local Similarity 100.0%; Pred. No. 1.6e-21;			
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	42 KRYTHGRGFTTKAINSCHTSSLATPEDKE 70		

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OM protein - protein search, using sw model

Run on: September 13, 2004, 12:27:50 ; Search time 32 Seconds
(without alignments)
321.049 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 199
Sequence: 1 LPICPGGAACQVTLRDLEF.....HKIDNYLKLLKRIIHNMC 199

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	199	100.0	351	1	US-08-196-350-1	Sequence 1, Appli
3	68	34.2	125	3	US-08-985-526-25	Sequence 25, Appl
4	68	34.2	253	3	US-08-985-526-27	Sequence 27, Appl
5	26	13.1	199	3	US-08-737-248-10	Sequence 10, Appl
6	26	13.1	199	3	US-08-737-248-12	Sequence 12, Appl
7	26	13.1	199	3	US-08-737-248-14	Sequence 14, Appl
8	25	12.6	199	3	US-08-737-248-8	Sequence 8, Appli
9	24	12.1	197	3	US-08-737-248-17	Sequence 17, Appl
10	24	12.1	198	3	US-08-737-248-6	Sequence 6, Appli
11	19	9.5	199	3	US-08-737-248-2	Sequence 2, Appli
12	19	9.5	426	3	US-08-737-248-4	Sequence 4, Appli
13	14	7.0	197	3	US-08-737-248-15	Sequence 15, Appl
14	13	6.5	197	3	US-08-737-248-16	Sequence 16, Appl
15	12	6.0	199	3	US-08-737-248-5	Sequence 5, Appli
16	12	6.0	199	3	US-08-737-248-11	Sequence 11, Appl
17	12	6.0	199	3	US-08-737-248-13	Sequence 13, Appl
18	10	5.0	188	3	US-08-737-248-20	Sequence 20, Appl
19	10	5.0	199	3	US-08-737-248-9	Sequence 9, Appli
20	8	4.0	8	2	US-08-669-284B-28	Sequence 28, Appl
21	8	4.0	8	3	US-09-190-964-13	Sequence 13, Appl
22	8	4.0	177	3	US-08-737-248-21	Sequence 21, Appl
23	8	4.0	187	3	US-08-737-248-18	Sequence 18, Appl
24	8	4.0	187	3	US-08-737-248-19	Sequence 19, Appl
25	7	3.5	163	4	US-09-252-991A-18617	Sequence 18617, A
26	7	3.5	165	4	US-09-519-232-44	Sequence 44, Appl
27	7	3.5	207	1	US-07-656-566-2	Sequence 2, Appli

28 7 3.5 212 4 US-09-134-000C-4518 Sequence 4518, Ap
29 7 3.5 231 1 US-07-656-566-3 Sequence 3, Appli
30 7 3.5 238 4 US-09-145-828A-13 Sequence 13, Appl
31 7 3.5 238 4 US-09-903-456-20 Sequence 20, Appl
32 7 3.5 301 1 US-08-393-985-12 Sequence 12, Appl
33 7 3.5 347 1 US-08-118-270-47 Sequence 47, Appl
34 7 3.5 347 5 PCT-US93-08528-47 Sequence 47, Appl
35 7 3.5 369 2 US-08-951-148-8 Sequence 8, Appli
36 7 3.5 369 2 US-09-165-234-8 Sequence 8, Appli
37 7 3.5 369 3 US-09-274-570-8 Sequence 8, Appli
38 7 3.5 466 4 US-09-489-039A-7654 Sequence 7654, Ap
39 7 3.5 511 4 US-09-540-236-2979 Sequence 2979, Ap
40 7 3.5 529 4 US-09-328-352-5413 Sequence 5413, Ap
41 7 3.5 591 4 US-09-519-232-66 Sequence 2979, Ap
42 7 3.5 943 4 US-09-397-885-5 Sequence 66, Appl
43 7 3.5 943 4 US-09-969-362-5 Sequence 5, Appli
44 7 3.5 1305 4 US-08-864-785-3 Sequence 3, Appli
45 7 3.5 1353 3 US-08-894-173-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-737-248-7
; Sequence 7, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
; APPLICANT: Guemene, Daniel
; APPLICANT: Zadworny, David
; APPLICANT: Karatzas, Costas
; TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
; TREATING BIRD BROODINESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,248
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR95/00576
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/05550
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6411P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-737-248-7

Query Match 100.0%; Score 199; DB 3; Length 199;

Best Local Similarity 100.0%; Pred. No. 4,4e-192;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LPICPGGAARCVTLRDLFDRAVVLGHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60

QY 61 SSLATPEDEKQAQOMNKKDFLSLIVSILRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 120
Db 61 SSLATPEDEKQAQOMNKKDFLSLIVSILRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 120

QY 121 EQTKRLLEGNELIVSQVHPETKENEIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRDHS 180
Db 121 EQTKRLLEGNELIVSQVHPETKENEIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRDHS 180

QY 181 KIDNYLKLKCRIIHNHNC 199
Db 181 KIDNYLKLKCRIIHNHNC 199

RESULT 2

US-08-196-350-1
; Sequence 1, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Moschicki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brad Salcedo
; STREET: One Kendall Square
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gosz, William G
; REGISTRATION NUMBER: 27,787
; REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELEPHONE: 6172527868
; TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human prolactin
US-08-196-350-1

Query Match 100.0%; Score 199; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 7,4e-192;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPICPGGAARCVTLRDLFDRAVVLGHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
Db 153 LPICPGGAARCVTLRDLFDRAVVLGHYIHLNLSSEMFSEFDKRYTHGRGFITKAINSCHT 212

QY 61 SSLATPEDEKQAQOMNKKDFLSLIVSILRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 120
Db 213 SSLATPEDEKQAQOMNKKDFLSLIVSILRSWNEPLYHLVTEVRGMOEAPAILSKAVEIE 272

QY 121 EQTKRLLEGNELIVSQVHPETKENEIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRDHS 180
Db 273 EQTKRLLEGNELIVSQVHPETKENEIYPVWSGLPSIQMADEESRLSAYYNLLHCLRRDHS 332

QY 181 KIDNYLKLKCRIIHNHNC 199
Db 333 KIDNYLKLKCRIIHNHNC 351

RESULT 3

US-08-985-526-25
; Sequence 25, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr, Robert G
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-25

Query Match 34.2%; Score 68; DB 3; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.2e-60;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 102 VRGMQEAP 109
Db 103 VRGMQEAP 110

RESULT 4

US-08-985-526-27
; Sequence 27, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 13:22:23 ; Search time 4225 Seconds
(without alignments)
2041.483 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
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Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1043	100.0	1071	6	AX014109	Sequence
7	1043	100.0	1071	6	BD204679	Human nuc
8	1043	100.0	1100	6	I31987	Sequence 2
9	1043	100.0	1388	9	BC015850	Homo sapi
10	1043	100.0	3541	6	E00953	Plasmid for
11	1036	99.3	807	9	HUMPRLA	M29386 Human prola
12	1036	99.3	5278	6	E02430	E02430 DNA encodin
13	1033	99.0	807	9	HUMPRLD	D00411 Homo sapien
14	1020	97.8	1150	9	MMU09018	Macaca mula
15	885	84.9	574	9	HSU75583	Homo sapien
16	879	84.3	868	4	AY373339	Equus cab
17	878	84.2	690	4	AY161285	Aluropod
18	877	84.1	841	4	SSPPLAC	Porcine mRN
19	874	83.8	880	4	OCU27199	Oryctolagus
20	867	83.1	884	4	FCU25974	Felis catus
21	857	82.2	862	4	AF054634	Trichosur
22	852	81.7	713	4	MVRNAP	M.vison gen
23	847	81.2	854	4	AF067726	Monodelph
24	838	80.3	892	3	THY457817	Taenia hy
25	803	77.0	864	4	AY373035	Cervus el
26	798	76.5	847	4	CHCPRNA	C.hircus ca
27	797	76.4	907	4	BTACT	Bos taurus
28	797	76.4	3549	6	E00955	Flasmid for
29	796	76.3	847	4	CHMGF1	C.hircus ca
30	796	76.3	880	4	OALHR	Sheep mRNA
31	794	76.1	926	4	SHPPRL	O.aries ovi
32	790	75.7	847	4	OAMGRNA	O.aries ovi
33	772	74.0	682	4	MVPROLAC	Mustela vis
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35	754	72.3	600	6	AR110193	Sequence
36	754	72.3	924	5	MGPLAC	Turkey mRNA
37	754	72.3	1281	6	A47307	Sequence 2
38	754	72.3	1281	6	AR110194	Sequence
39	752	72.1	702	5	AY332494	Ambystoma
40	748	71.7	953	5	CHKPRL	Chicken pro
41	748	71.7	953	5	MGU05952	Meleagris g
42	748	71.7	978	6	E02259	cDNA encodi
43	701	67.2	908	5	XELPRL	prolac
44	690.5	66.2	899	5	RCPROLACT	R.cartesbei
45	667	64.0	900	6	E03099	DNA encodin

ALIGNMENTS

Db 629 AAAATCGCAATTAATCTCAAGCTCTTGAAGTGGCGAATCATCCACAACAACAACTGC 685

RESULT 2

HSLACT

LOCUS Homo sapiens mRNA 833 bp mRNA linear PRI 21-OCT-2003

DEFINITION V00566 J00299 Homo sapiens mRNA for prolactin.

ACCESSION V00566.1 GI:34210

VERSION prolactin.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 833)

AUTHORS Cooke,N.E., Coit,D., Shine,J., Baxter,J.D. and Martial,J.A.

TITLE Human prolactin. cDNA structural analysis and evolutionary comparisons

JOURNAL J. Biol. Chem. 256 (8), 4007-4016 (1981)

MEDLINE 81168179

PUBMED 6260780

COMMENT On Sep 5, 2003 this sequence version replaced gi:190353.

FEATURES

source

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Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 4.43e-98 Length: 833

Score: 1043.00 Matches: 199

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-10-735-594-1 (1-199) x HSLACT (1-833)

Qy 1 LeuProfileCysProGlyGlyAlaAlaAatqCysGlnValThrLeuArgAspLeuPheAsp 20

Db 89 TTGCGCCATGTCTCCCGCGGGGTGCCCGATGCCAGTGACCTTCAGACCTGTTTGAC 148

Qy 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40

Db 149 CGGCGCGTCTGCTGTCTCCCACTACATCCATCACTCTCTCCAGAAATGTTTCAGCAATTC 208

Qy 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60

Db 209 GATAAAGCGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 268

Qy 61 SerSerLeuAlaThrProGluAspLysGluAlaGlnGlnMetAsnGlnLysAspPhe 80

Db 269 TCATTCCCTTGCACCCCGAAGACAGAGACAGCCCAACAGATGAATCAAAAGACTTT 328

Qy 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100

Db 329 CTGAGCTGATAGTCACATATTGCATCTTGAATCAGCTCTGTATCATCTGTCACG 388

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 15:00:54 ; Search time 2733 Seconds
(without alignments)
2174.378 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPTCPGAGRCQVTLRDLEF.....HKIDNVLLKLCRIHHNNC 199

Scoring table:
BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1043	100.0	740	14	CD239100	CD239100 FNPBKE08
2	1043	100.0	741	14	CD239111	CD239111 FNPBKE09
3	1043	100.0	747	14	CD239635	CD239635 FNPBKG10
4	1043	100.0	749	14	CD239093	CD239093 FNPBKD11
5	1043	100.0	749	14	CD239460	CD239460 FNPBUG08
6	1043	100.0	764	14	CD519470	CD519470 AGENCOURT
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DEFINITION FNPBKE08 FNP Homo sapiens cdna, mRNA sequence.
ACCESSION CD239100
VERSION CD239100.1 GI:30982565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Ma, Y., Qi, X., Zhang, X., Xiao, H., Zhu, Z., Yan, Q., Chen, Z. and Han, Z.

TITLE Fetal Pituitary ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.

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Query Match: 100.00% Indels: 0
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VERSION CD239111.1 GI:30982576
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SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.
Fetal Pituitary ESTs
Unpublished (2003)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.

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QY 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluLeuGlu 120
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GenCore version 5.1.6
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(without alignments)

1380.440 Million cell updates/sec

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Maximum Match 100%
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5	641	61.5	390	3	Sequence 3, Appli
6	641	61.5	771	3	Sequence 26, Appl
7	263	25.2	933	3	Sequence 28, Appl
8	245.5	23.5	887	3	Sequence 1, Appli
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16	190	18.2	579	1	US-07-885-689A-36	Sequence 36, Appl
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24	184	17.6	596	1	US-09-280-030-52	Sequence 52, Appl
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ALIGNMENTS

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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
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TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1416:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 970 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: G531102
 US-09-016-434-1416

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RESULT 2

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 Patent No. 5585099
 GENERAL INFORMATION:
 APPLICANT: Richards, Sue
 APPLICANT: Kaplan, Joanne
 APPLICANT: Mosciacki, Richard
 TITLE OF INVENTION: PROLACTIN AS ADJUVANT
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:

ADDRESS: Brad Salcedo
 STREET: One Kendall Square
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02139
 COMPUTER READABLE FORM:
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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
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 APPLICATION NUMBER: US/08/196,350
 FILING DATE: 08/08/1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Gosz, William G
 REGISTRATION NUMBER: 27,787
 REFERENCE/DOCKET NUMBER: GEN 4-1.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 61752527868
 TELEFAX: 6173747225
 INFORMATION FOR SEQ ID NO: 2:
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 MOLECULE TYPE: cDNA
 US-08-196-350-2

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Word size: 1

Total number of hits satisfying chosen parameters: 6934743

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	199	100.0	833	6	AX587623	AX587623 Sequence
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4	199	100.0	970	6	AR270853	AR270853 Sequence
5	199	100.0	970	9	HSPRO205	X54393 H.sapiens m
6	199	100.0	1071	6	AX014109	AX014109 Sequence
7	199	100.0	1071	6	BD204679	BD204679 Human nuc
8	199	100.0	1100	6	I31987	I31987 Sequence 2
9	199	100.0	1388	9	BC015850	BC015850 Homo sapi
10	199	100.0	3541	6	E00953	E00953 Plasmid for
11	185	93.0	5278	6	E02430	E02430 DNA encodin
12	177	88.9	807	9	HUMPRLA	M29386 Human prola
13	124	62.3	390	6	AR100635	AR100635 Sequence
14	124	62.3	390	6	E34066	E34066 Carrier/DNA
15	124	62.3	771	6	AR100636	AR100636 Sequence
16	124	62.3	771	6	E34067	E34067 Carrier/DNA
17	123	61.8	387	6	AX824654	AX824654 Sequence
18	123	61.8	756	6	AX824656	AX824656 Sequence
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24	61	30.7	675	9	HSPROL6	X00543 H.sapiens g
25	52	26.1	1150	9	MMU09018	U09018 Macaca mula
26	40	20.1	329	9	HSPRO204	X54394 H.sapiens p
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28	40	20.1	156690	2	AC027163	AC027163 Homo sapi
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33	25	12.6	882	4	MVPROLAC	X63235 Mustela vis
34	25	12.6	690	4	AY161285	AY161285 Alluropod
35	25	12.6	713	4	MVRNAP	X59785 M.vison gen
36	25	12.6	868	4	AY373339	AY373339 Equus cab
37	25	12.6	903	4	AY249860	AY249860 Mustela v
38	24	12.1	585	5	S69309	S69309 prolactin {
39	24	12.1	854	4	AF067726	AF067726 Monodelph
40	24	12.1	862	4	AF054634	AF054634 Trichosur
41	24	12.1	899	5	RCPROLACT	X10663 R.cartesbei
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ALIGNMENTS

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 DEFINITION Sequence 93 from Patent WO0246467.
 ACCESSION AX587623
 VERSION AX587623.1 GI:28212349
 KEYWORDS synthetic construct
 SOURCE synthetic sequences
 ORGANISM
 REFERENCE 1 Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P. and Fert, V.
 AUTHORS Gene expression profiling of primary breast carcinomas using arrays of candidate genes
 TITLE Patent: WO 0246467-A 93 13-JUN-2002;
 JOURNAL Ipsogen (FR)
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 Query Match: 100.00% Indels: 0
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 QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
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 ACCESSION V00566 J00299
 VERSION V00566.1 GI:34210
 KEYWORDS prolactin.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Cooke, N.E., Coit, D., Shine, J., Baxter, J.D. and Martial, J.A.
 TITLE Human prolactin. cDNA structural analysis and evolutionary comparisons
 JOURNAL J. Biol. Chem. 256 (8), 4007-4016 (1981)
 MEDLINE 81168179
 PUBMED 6260780
 COMMENT On Sep 5, 2003 this sequence version replaced gi:190353.
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 Pred. No.: 1.81e-198 Length: 833
 Score: 199.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-10-735-594-1 (1-199) x HSLACT (1-833)
 QY 1 LeuProleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
 Db 89 TTGCCCATCTGTCCCGGGGGTGGCCGATGCCAGTGACCCCTTCAGACCTGTTTGAC 148
 QY 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
 Db 149 CGCGCGCTGCTCTGCCACTACATCAATCAATCTCTCAGAAATGTTTCAGCGAATTC 208
 QY 41 AsplysArgTyrThrHisGlyArgGlyPheIleThrIysAlaIleAsnSerCysHisThr 60
 Db 209 GATAAAGCGTATACCATTCGCGGGGTTCATTACCAAGGCCATCAACAGCTGCCACCT 268
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 Db 269 TCTTCCCTTGCACCCCGAGACAGAGCAGCCACAGATGAATCAAAAGACTTT 328
 QY 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
 Db 329 CTGAGCCTGATAGTCAGCATATTGCGATCTCGAATGAGCTCTGTATCATCTGGTCAGC 388

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 19:12:35 ; Search time 2734 Seconds
(without alignments)
2173.592 Million cell updates/sec

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Word size: 1

Total number of hits satisfying chosen parameters: 55025477

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptp
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	199	100.0	741	14	CD239111	CD239111 FNPBKF09
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4	199	100.0	749	14	CD239093	CD239093 FNPBKD11
5	199	100.0	749	14	CD239460	CD239460 FNPBVG08
6	199	100.0	764	14	CD519470	CD519470 AGENCOURT
7	199	100.0	810	14	CD251429	CD251429 AGENCOURT
8	199	100.0	813	14	CD251266	CD251266 AGENCOURT
9	199	100.0	816	14	CD106943	CD106943 AGENCOURT
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ALIGNMENTS

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ACCESSION CD239100.1 GI:30982565
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.

TITLE Fetal Pituitary ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.

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DB 616 GAAGAGTCTGCCCTTCTGCTTATTAACCTGTCTCCACTGCCCTACCGAGGATTCACAT 675
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RESULT 2

CD239111

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DEFINITION FNP Homo sapiens cDNA, mRNA sequence.
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VERSION CD239111.1 GI:30982576
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.
TITLE Fetal Pituitary ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.

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Query Match: 100.00% Indels: 0
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DB 258 GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 317
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DB 438 GAAGTACGTGGTATGCAAGAGCCCGGAGGCTATCTCTATCAAGCTGTAGAGATTGAG 497
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DB 498 GAGCAACCAACCGCTTCTAGAGGCGATGGAGCTGATGATCAGCCAGGTTTCCTCGAA 557
QY 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
DB 558 ACCAAAGAAATGAGATCTACCCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT 617
QY 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgAspSerHis 180

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: September 13, 2004, 19:20:35 ; Search time 80 Seconds
(without alignments)
1380.440 Million cell updates/sec

Title: US-10-735-594-1

Perfect score: 199

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Fgapop 6.0 , Fgapext 7.0
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Searched: 682709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	19	9.5	600	3	US-08-737-248-1
6	19	9.5	1281	3	US-08-737-248-3
C 7	9	4.0	269223	4	US-09-596-002-41
C 8	8	4.0	26	4	US-09-058-333A-65
C 9	7	3.5	38	2	US-07-829-461A-24
C 10	7	3.5	38	3	US-09-197-649-25
C 11	7	3.5	48	2	US-07-829-461A-22
C 12	7	3.5	48	3	US-09-197-649-23

13	7	3.5	187	3	US-08-903-446A-11	Sequence 11, Appl
C 14	7	3.5	305	4	US-09-702-705-131	Sequence 131, App
C 15	7	3.5	305	4	US-09-736-457-131	Sequence 131, App
C 16	7	3.5	305	4	US-09-614-124B-131	Sequence 131, App
C 17	7	3.5	305	4	US-09-671-325-131	Sequence 131, App
C 18	7	3.5	305	4	US-09-589-184-131	Sequence 1280, Ap
C 19	7	3.5	307	4	US-09-702-705-1280	Sequence 1280, Ap
C 20	7	3.5	307	4	US-09-702-705-1440	Sequence 1440, Ap
C 21	7	3.5	307	4	US-09-736-457-1280	Sequence 1280, Ap
C 22	7	3.5	307	4	US-09-736-457-1440	Sequence 1440, Ap
C 23	7	3.5	307	4	US-09-614-124B-1280	Sequence 1280, Ap
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C 25	7	3.5	307	4	US-09-671-325-1280	Sequence 1280, Ap
C 26	7	3.5	307	4	US-09-671-325-1440	Sequence 1440, Ap
C 27	7	3.5	371	4	US-09-684-385-3	Sequence 3, Appli
C 28	7	3.5	407	4	US-09-221-017B-831	Sequence 831, App
C 29	7	3.5	436	4	US-09-621-976-16375	Sequence 16375, A
C 30	7	3.5	446	4	US-09-621-976-18136	Sequence 18136, A
C 31	7	3.5	476	4	US-09-621-976-3529	Sequence 3529, Ap
C 32	7	3.5	489	4	US-09-679-409-78	Sequence 78, Appl
C 33	7	3.5	492	4	US-09-252-991A-2046	Sequence 2046, Ap
C 34	7	3.5	498	4	US-09-519-232-43	Sequence 43, Appl
C 35	7	3.5	520	4	US-08-936-165A-13	Sequence 13, Appl
C 36	7	3.5	612	4	US-09-766-055A-3	Sequence 3, Appli
C 37	7	3.5	615	4	US-09-107-532A-813	Sequence 813, App
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C 40	7	3.5	696	1	US-07-656-566-4	Sequence 4, Appli
C 41	7	3.5	733	4	US-09-327-983-11	Sequence 11, Appl
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C 43	7	3.5	780	4	US-09-252-991A-15360	Sequence 15360, A
C 44	7	3.5	831	4	US-09-118-554-66	Sequence 66, Appl
C 45	7	3.5	831	4	US-09-118-627-66	Sequence 66, Appl

ALIGNMENTS

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; Sequence 1416, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555

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; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1416:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G531102
US-09-016-434-1416

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; Sequence 2, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Morsicki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Brad Salcedo
; STREET: One Kendall Square
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,350
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gosz, William G
; REGISTRATION NUMBER: 27,787
; REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 6172527868
; TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-196-350-2

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GenCore version 5.1.1.6
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SUMMARIES

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5	199	100.0	1062	16	US-10-291-172-38	Sequence 38, Appl
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9	177	88.9	603	17	US-10-714-067-1	Sequence 1, Appli
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17	81	40.7	603	10	US-09-819-094-4	Sequence 4, Appli
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23	13	6.5	48	15	US-10-153-207-18	Sequence 18, Appl
24	13	6.5	443	15	US-10-007-926A-91	Sequence 91, Appl
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34	12	6.0	357	9	US-09-960-352-2417	Sequence 2417, Ap
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36	12	6.0	363	9	US-09-960-352-6004	Sequence 6004, Ap
37	12	6.0	368	9	US-09-960-352-3831	Sequence 3831, Ap
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41	12	6.0	393	9	US-09-960-352-11400	Sequence 11400, A
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45	12	6.0	410	9	US-09-960-352-778	Sequence 778, App

ALIGNMENTS

RESULT 1

US-10-140-293-1

; Sequence 1, Application US/10140293

; Publication No. US20030022833A1

; GENERAL INFORMATION:

; APPLICANT: CHEN, WEN Y.

; APPLICANT: WAGNER, THOMAS E.

; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE

; TITLE OF INVENTION: CONDITIONS

; FILE REFERENCE: 035879/0109

; CURRENT APPLICATION NUMBER: US/10/140,293

; CURRENT FILING DATE: 2002-05-08

; PRIOR APPLICATION NUMBER: US/09/246,041

; PRIOR FILING DATE: 1999-02-05

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 1

; LENGTH: 684

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-140-293-1

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Db 145 CGCCCGTGCCTGTCCTCCCATACATCAATAACCTCTCTCAGAAATGTTTTCAGCAATTC 204

Qy 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 205 GATAAACGGTATACCCATGCGCGGGGTTCTATTACCAAGGCCATCAACAGCTGCACACT 264

Qy 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
Db 265 TCTTCCCTTGCCACCCCGAAGCAAGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 324

Qy 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
Db 325 CTGAGCCTGATGAGCAGATATTCGATCTCGGAATGAGCTCTGTATCATCTGTCACG 384

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db 385 GAAGTACGTGATGCAAGAGCCCGGAGGCTATCTATCAAAAGCTGTAGAGATTGAG 444

Qy 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db 445 GAGCAAAACCAACCGCTTCTAGAGGCGATGGAGCTGATAGTCAGCCAGGTTTCATCTGAA 504

Qy 141 ThrLysGluAsnGluIleTyrProValTyrSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db 505 ACCAAAGAAATAGATCTACCTGTCTGGTGGGACTTCATCCCTGCAGATGGCTGAT 564

Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgAspSerHis 180
Db 565 GAAGAGTCTGCTTCTGCTTATTATTAACCTGTCTCCACTGCCATCCAGGGATTTCACAT 624

Qy 181 LysLeuAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
Db 625 AAAATCGACATATTATCTCAAGCTCCTGAAAGTGGCGGAATCATCCCAACAACACTGC 681

RESULT 2

US-10-007-926A-93
; Sequence 93, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BURNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1946-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: prolactin (PRL) gene.
US-10-007-926A-93

Alignment Scores: 4,91e-202 Length: 833
Pred. No.: 199.00 Matches: 199
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-735-594-1 (1-199) x US-10-007-926A-93 (1-833)

Qy 1 LeuProLeuCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
Db 89 TTGCCCATCTGTCCTCCCGGGGGTCCCGGATGCCAGGTGACCTTCAGACCTGTTTGAC 148

Qy 21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db 149 CGCCCGTGCCTGTCCTCCCATACATCAATAACCTCTCTCAGAAATGTTTTCAGCAATTC 208

Qy 41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db 209 GATAAACGGTATACCCATGCGCGGGGTTCTATTACCAAGGCCATCAACAGCTGCACACT 268

Qy 61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnMetAsnGlnLysAspPhe 80
Db 269 TCTTCCCTTGCCACCCCGAAGCAAGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 328

Qy 81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
Db 329 CTGAGCCTGATGAGCAGATATTCGATCTCGGAATGAGCTCTGTATCATCTGTCACG 388

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db 389 GAAGTACGTGATGCAAGAGCCCGGAGGCTATCTATCAAAAGCTGTAGAGATTGAG 448

Qy 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db 449 GAGCAAAACCAACCGCTTCTAGAGGCGATGGAGCTGATAGTCAGCCAGGTTTCATCTGAA 508

Qy 141 ThrLysGluAsnGluIleTyrProValTyrSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db 509 ACCAAAGAAATAGATCTACCTGTCTGGTGGGACTTCATCCCTGCAGATGGCTGAT 568

Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgAspSerHis 180
Db 569 GAAGAGTCTGCTTCTGCTTATTATTAACCTGTCTCCACTGCCATCCAGGGATTTCACAT 628

Qy 181 LysLeuAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
Db 629 AAAATCGACATATTATCTCAAGCTCCTGAAAGTGGCGGAATCATCCCAACAACACTGC 685

RESULT 3

US-10-305-720-1416
; Sequence 1416, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1416
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: